

FIGURE 1

GGCTGAGGGGAGGCCCGGAGCCTTTCTGGGGCCTGGGGGATCCTCTTGCACTGGTGGGTGGA
GAGAAGCGCCTGCAGCCAACCAGGGTCAGGCTGTGCTCACAGTTTCCTCTGGCGGCATGTAA
AGGCTCCACAAAGGAGTTGGGAGTTCAAATGAGGCTGCTGCGGACGGCCTGAGGATGGACCC
CAAGCCCTGGACCTGCCGAGCGTGGCACTGAGGCAGCGGCTGACGCTACTGTGAGGGGAAAGA
AGGTTGTGAGCAGCCCCGAGGACCCCTGGCCAGCCCTGGCCCCAGCCTCTGCCGGAGCCCT
CTGTGGAGGCAGAGCCAGTGGAGCCAGTGGAGGCAGGGCTGCTTGGCAGCCACCGGCCTGCA
ACTCAGGAACCCCTCCAGAGGCCATGGACAGGCTGCCCCGCTGACGGCCAGGGTGAAGCATG
TGAGGAGCCGCCCCGGAGCCAAGCAGGAGGGAAGAGGCTTTCATAGATTCTATTACAAAGA
ATAACCACCATTTTGCAAGGACC**ATG**AGGCCACTGTGCGTGACATGCTGGTGGCTCGGACTG
CTGGCTGCCATGGGAGCTGTTGCAGGCCAGGAGGACGGTTTTGAGGGGCACTGAGGAGGGCTC
GCCAAGAGAGTTTCAATTTACCTAAACAGGTACAAGCGGGCGGGCGAGTCCCAGGACAAGTGCA
CCTACACCTTCATTGTGCCCCAGCAGCGGGTCACGGGTGCCATCTGCGTCAACTCCAAGGAG
CCTGAGGTGCTTCTGGAGAACCGAGTGCATAAGCAGGAGCTAGAGCTGCTCAACAATGAGCT
GCTCAAGCAGAAGCGGCAGATCGAGACGCTGCAGCAGCTGGTGGAGGTGGACGGCGGCATTG
TGAGCGAGGTGAAGCTGCTGCGCAAGGAGAGCCGCAACATGAACCTCGCGGGTACACGAGCTC
TACATGCAGCTCCTGCACGAGATCATCCGCAAGCGGGACAACGCGTTGGAGCTCTCCAGCT
GGAGAACAGGATCCTGAACCAGACAGCCGACATGCTGCAGCTGGCCAGCAAGTACAAGGACC
TGGAGCACAAGTACCAGCACCTGGCCACACTGGCCCACAACCAATCAGAGATCATCGCGCAG
CTTGAGGAGCACTGCCAGAGGGTGGCCTCGGCCAGGCCCCGTCCCCAGCCACCCCCCGCTGC
CCCGCCCCGGGTCTACCAACCACCCACCTACAACCGCATCATCAACCAGATCTCTACCAACG
AGATCCAGAGTGACCAGAACCTGAAGGTGCTGCCACCCCCCTCTGCCCACTATGCCCACTCTC
ACCAGCCTCCCATCTTCCACCGACAAGCCGTGGGGCCATGGAGAGACTGCCTGCAGGCCCT
GGAGGATGGCCACGACACCAGCTCCATCTACCTGGTGAAGCCGGAGAACACCAACCGCCTCA
TGCAGGTGTGGTGCGACCAGAGACACGACCCCGGGGGCTGGACCGTCATCCAGAGACGCCTG
GATGGCTCTGTAACTTCTTCAGGAAGTGGGAGACGTACAAGCAAGGGTTTGGGAACATTGA
CGGCGAATACTGGCTGGGCCTGGAGAACATTTACTGGCTGACGAACCAAGGCAACTACAAAC
TCCTGGTGACCATGGAGGACTGGTCCGGCCGCAAAGTCTTTGCAGAATACGCCAGTTTCCGC
CTGGAACCTGAGAGCGAGTATTATAAGCTGCGGCTGGGGCGCTACCATGGCAATGCGGGTGA
CTCCTTTACATGGCACAACGGCAAGCAGTTCACCACCCTGGACAGAGATCATGATGTCTACA
CAGGAAACTGTGCCCACTACCAGAAGGGAGGCTGGTGGTATAACGCCTGTGCCCACTCCAAC
CTCAACGGGGTCTGGTACCGCGGGGGCCATTACCGGAGCCGCTACCAGGACGGAGTCTACTG
GGCTGAGTTCCGAGGAGGCTCTTACTCACTCAAGAAAGTGGTGATGATGATCCGACCGAACC
CCAACACCTTCCAC**TAAG**CCAGCTCCCCCTCCTGACCTCTCGTGGCCATTGCCAGGAGCCCA
CCCTGGTCACGCTGGCCACAGCACAAAGAACAACCTCCTCACCAGTTCATCCTGAGGCTGGGA
GGACCGGGATGCTGGATTCTGTTTTCCGAAGTCACTGCAGCGGATGATGGAAGTGAATCGAT
ACGGTGTTTTCTGTCCCTCCTACTTTCTTACACACAGACAGCCCCCTCATGTCTCCAGGACA
GGACAGGACTACAGACAACCTCTTTCTTTAAATAAATTAAGTCTCTACAATAAAAAAA

FIGURE 2

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA22779
><subunit 1 of 1, 493 aa, 1 stop
><MW: 57104, pI: 7.67, NX(S/T): 2
MRPLCVTCWWLGLLAAMGAVAGQEDGFEGTEEGSPREFIYLNRYKRAGESQDKCTYTFIVPQ
QRVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQKRQIETLQQLVEVDGGIVSEVKLLR
KESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRILNQADMLQLASKYKDLEHKYQHL
ATLAHNQSEIIAQLEEHCCQRVPSARPVPQPPPAAPPRVYQPPTYNRIINQISTNEIQSDQNL
KVLPPPLPTMPTLTSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTNRLMQVWCDQR
HDPGGWTVIQRRLDGSVNFERNWETKYQGFGNIDGEYWLGLENIYWLTNQGNKYKLLVTMEDW
SGRKVF AEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLD RDHDVYTGNCAHYQ
KGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKKVMMIRPNPNTFH
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Important features of the protein:**Signal peptide:**

amino acids 1-22

N-glycosylation sites.

amino acids 164-168, 192-196

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 124-128

Tyrosine kinase phosphorylation sites.

amino acids 177-184, 385-393, 385-394, 461-468

N-myristoylation sites.amino acids 12-18, 18-24, 22-28, 29-35, 114-120, 341-347,
465-471, 473-479**Amidation site.**

amino acids 373-377

Fibrinogen beta and gamma chains C-terminal domain signature.

amino acids 438-451

Fibrinogen beta and gamma chains C-terminal domain proteins.

amino acids 305-343, 365-402, 411-424, 428-458

Trehalase proteins.

amino acids 275-292

CCACGCGTCCGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCAAAA
GGAGTCGCGCCCGCCGCCGCCGCCCTCCCTCCGGTGGGCCCCGGGAGGTAGAGAAAGTCAGT
GCCACAGCCCGACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCTGAGGGT
TGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACCGGACTGGG
GCCGGGGTAGGCTCTGGAAAGGGCCCCGGGAGAGAGGTGGCGTTGGTCAGAACCTGAGAAACA
GCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTCTAGAGAGGGT
GTTCCCTCTTTGCGGGGTCCTCACCAGAAGAGGTTCTTGGGGGTCGCCCTTCTGAGGAGGCT
GCGGCTAACAGGGCCCAGAACTGCCATTGGATGTCCAGAATCCCCTGTAGTTGATAATGTTG
GGAATAAGCTCTGCAACTTTCTTTGGCATTTCAGTTGTTAAAAACAAATAGGATGCAAATTCC
TCAACTCCAGGTTATGAAAACAGTACTTGGAACCTGAAACCTACCTAAATGATCGTCTTTG
GTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGGCCAGGGTCTGTTGTTGACTCTCGAAGAG
CACATAGCCCCTTCCTAGGGACTGGAGGTGCCGCTACTACCATGGGTAATTCTGTATCTG
CCGAGATGACAGTGGAACAGATGACAGTGTTGACACCCAACAGCAACAGGCCGAGAACAGTG
CAGTACCCACTGCTGACACAAGGAGCCAACCACGGGACCCTGTTGCGCCACCAAGGAGGGGC
CGAGGACCTCATGAGCCAAGGAGAAAGAAACAAAATGTGGATGGGCTAGTGTTGGACACACT
GGCAGTAATACGGACTCTTGTAGATAAGTAAGTATCTGACTCACGGTCACCTCCAGTGGAAT
GAAAAGTGTTCTGCCCCGAACCATGACTTTAGGACTCCTTCAGTTCCTTTAGGACATACTCG
CCAAGCCTTGTGCTCACAGGGCAAAGGAGAATATTTTAATGCTCCGCTGATGGCAGAGTAAA
TGATAAGATTTGATGTTTTTGCTTGCTGTCATCTACTTTGTCTGGAAATGTCTAAATGTTTC
TGTAGCAGAAAACACGATAAAGCTATGATCTTTATTAGAG

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FIGURE 4

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA26846

<subunit 1 of 1, 117 aa, 1 stop

<MW: 12692, pI: 7.50, NX(S/T): 0

MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQQQ

AENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNVDGLVLDLAVIRTLVDK

Important features:

Signal peptide:

amino acids 1-16

N-myristoylation sites.

amino acids 18-24, 32-38, 34-40, 35-41, 51-57

FIGURE 5

CCCACGCGTCCGCGCAGTCGCGCAGTTCTGCCTCCGCCTGCCAGTCTCGCCCCGCGATCCCCGG
CCCGGGGCTGTGGCGTCGACTCCGACCCAGGCAGCCAGCAGCCCCGCGCGGGAGCCGGACCGC
CGCCGGAGGAGCTCGGACGGCATGCTGAGCCCCCTCCTTTGCTGAAGCCCCGAGTGCGGAGAA
GCCCCGGGCAAACGCAGGCTAAGGAGACCAAAGCGGGCGAAGTCGCGGAGACAGCGGACAAGCAG
CGGAGGAGAAGGAGGAGGAGGCGAACCCAGAGAGGGGCAGCAAAGAAGCGGTGGTGGTGGG
CGTCGTGGCCATGGCGGCGGCTATCGCCAGCTCGCTCATCCGTCAGAAGAGGCAAGCCCCGCG
AGCGCGAGAAATCCAACGCCTGCAAGTGTGTCAGCAGCCCCAGCAAAGGCAAGACCAGCTGC
GACAAAAACAAGTTAAATGTCTTTTCCCGGGTCAAACCTCTTCGGCTCCAAGAAGAGGCGCAG
AAGAAGACCAGAGCCTCAGCTTAAGGGTATAGTTACCAAGCTATACAGCCGACAAGGCTACC
ACTTGCAGCTGCAGGCGGATGGAACCATTTGATGGCACCAAAGATGAGGACAGCACTTACACT
CTGTTTAACCTCATCCCTGTGGGTCTGCGAGTGGTGGCTATCCAAGGAGTTCAAACCAAGCT
GTACTTGGCAATGAACAGTGAGGGATACTTGTACACCTCGGAACTTTTTCACACCTGAGTGCA
AATTCAAAGAATCAGTGTTTGAAAATTATTATGTGACATATTCATCAATGATATACCGTCAG
CAGCAGTCAGGCCGAGGGTGGTATCTGGGTCTGAACAAAGAAGGAGAGATCATGAAAGGCAA
CCATGTGAAGAAGAACAAGCCTGCAGCTCATTTTCTGCCTAAACCACTGAAAGTGGCCATGT
ACAAGGAGCCATCACTGCACGATCTCACGGAGTTCTCCCGATCTGGAAGCGGGACCCCAACC
AAGAGCAGAAGTGTCTCTGGCGTGCTGAACGGAGGCAAATCCATGAGCCACAATGAATCAAC
GTAGCCAGTGAGGGCAAAGAAGGGCTCTGTAACAGAACCTTACCTCCAGGTGCTGTTGAAT
TCTTCTAGCAGTCCTTCACCCAAAAGTTCAAATTTGTCAGTGACATTTACCAAACAAACAGG
CAGAGTTCACTATTCTATCTGCCATTAGACCTTCTTATCATCCATACTAAAGC

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FIGURE 6

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA28498

><subunit 1 of 1, 245 aa, 1 stop

><MW: 27564, pI: 10.18, NX(S/T): 1

MAAAIASSLIRQKRQAREREKSNACKCVSSPSKGKTSCDKNKLNVFSRVKLFSGSKKRRRRRP
EPQLKGIIVTKLYSRQGYHLQLQADGTIDGTDKEDSTYTLFNLIPVGLRVVAIQGVQTKLYLA
MNSEGYLYTSELFTEPECKFKESVFENYYVTYSSMIYRQQQSGRGWYLGLNKEGEIMKGNHVK
KNKPAAHFLPKPLKVAMYKEPSLHDLTEFSRSGSGTPTKSRSVSGVLNGGKSMSHNEST

N-glycosylation site.

amino acids 242-246

Glycosaminoglycan attachment site.

amino acids 165-169, 218-222

Tyrosine kinase phosphorylation site.

amino acids 93-100

N-myristoylation site.

amino acids 87-93, 231-237

ATP/GTP-binding site motif A (P-loop).

amino acids 231-239

HBGF/FGF family proteins

amino acids 78-94, 102-153

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FIGURE 7

ATGGCCGCGGCCATCGCTAGCGGCTTGATCCGCCAGAAGCGGCAGGCGCGGGAGCAGCACTG
GGACCGGCCGTCTGCCAGCAGGAGGCGGAGCAGCCCCAGCAAGAACCGCGGGGCTCTGCAACG
GCAACCTGGTGGATATCTTCTCCAAAGTGCGCATCTTCGGCCTCAAGAAGCGCAGGTTGCGG
CGCCAAGATCCCCAGCTCAAGGGTATAGTGACCAGGTTATATTGCAGGCAAGGCTACTACTT
GCAAATGCACCCCGATGGAGCTCTCGATGGAACCAAGGATGACAGCACTAATTCTACACTCT
TCAACCTCATAACAGTGGGACTACGTGTTGTTGCCATCCAGGGAGTGAAAACAGGGTTGTAT
ATAGCCATGAATGGAGAAGGTTACCTCTACCCATCAGAACTTTTTACCCCTGAATGCAAGTT
TAAAGAATCTGTTTTTTGAAAATTATTATGTAATCTACTCATCCATGTTGTACAGACAACAGG
AATCTGGTAGAGCCTGGTTTTTTGGGATTAAATAAGGAAGGGCAAGCTATGAAAGGGAACAGA
GTAAAGAAAACCAAACCAGCAGCTCATTTTCTACCCAAGCCATTGGAAGTTGCCATGTACCG
AGAACCATCTTTGCATGATGTTGGGGAAACGGTCCCGAAGCCTGGGGTGACGCCAAGTAAAA
GCACAAGTGCGTCTGCAATAATGAATGGAGGCAAACCAGTCAACAAGAGTAAGACAACA**TAG**

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FIGURE 8

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA28503

><subunit 1 of 1, 247 aa, 1 stop

><MW: 27702, pI: 10.36, NX(S/T): 2

MAAAIASGLIRQKRQAREQHWDRPSASRRRSSPSKNRGLCNGNLVDIFSKVRIFGLKKRRLR
RQDPQLKGIIVTRL YCRQGY YLQMHPDGALDGTKDDSTNSTLFNLIPVGLRVVAIQGVKTGLY
IAMNGEGYLYPSELFTPECKFKESVFENYYVIYSSMLYRQQESGRAWFLGLNKEGQAMKGNR
VKKTKPAAHFLPKPLEVAMYREPSLHDVGETV PKPGVTPSKSTSASAIMNGGKPVNKS KTT

N-glycosylation site.

amino acids 100-104, 242-246

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 28-32, 29-33

Tyrosine kinase phosphorylation site.

amino acids 199-207

N-myristoylation site.

amino acids 38-44, 89-95, 118-124, 122-128, 222-228

HBGF/FGF family proteins.

amino acids 104-155, 171-198

FIGURE 9

CTCGCAGCCGAGCGCGGCCGGGGAAGGGCTCTCCTTCCAGCGCCGAGCACTGGGCCCTGGCA
GACGCCCCAAGATTGTTGTGAGGAGTCTAGCCAGTTGGTGAGCGCTGTAATCTGAACCAGCT
GTGTCCAGACTGAGGCCCATTTGCATTGTTTAACTACTTAGAAAATGAAGTGTTCATTTT
TAACATTCTCTCTCCAATTGGTTTAAATGCTGAATTACTGAAGAGGGCTAAGCAAAACCAGGT
GCTTGCGCTGAGGGCTCTGCAGTGGCTGGGAGGACCCCGGCGCTCTCCCCGTGTCTCTCCA
CGACTCGCTCGGCCCTCTGGAATAAAACACCCGCGAGCCCCGAGGGCCCCAGAGGAGGCCGA
CGTGCCCGAGCTCCTCCGGGGGTCCCGCCCGCGAGCTTTCTTCTCGCCTTCGCATCTCCTCC
TCGCGCGTCTTGACATGCCAGGAATAAAAAGGATACTCACTGTTACCATTCTGGCTCTCTG
TCTTCCAAGCCCTGGGAATGCACAGGCACAGTGCACGAATGGCTTTGACCTGGATCGCCAGT
CAGGACAGTGTGTAGATATTGATGAATGCCGAACCATCCCCGAGGCCTGCCGAGGAGACATG
ATGTGTGTTAACCAAAATGGCGGGTATTTATGCATTCCCCGGACAAACCCTGTGTATCGAGG
GCCCTACTCGAACCCCTACTCGACCCCTACTCAGGTCCGTACCCAGCAGCTGCCCCACCAC
TCTCAGCTCCAACTATCCCACGATCTCCAGGCCTCTTATATGCCGCTTTGGATACCAGATG
GATGAAAGCAACCAATGTGTGGATGTGGACGAGTGTGCAACAGATTCCCACCAGTGCAACCC
CACCCAGATCTGCATCAATACTGAAGGCGGGTACACCTGCTCCTGCACCGACGGATATTGGC
TTCTGGAAGGCCAGTGCTTAGACATTGATGAATGTGCTATGGTTACTGCCAGCAGCTCTGT
GCGAATGTTCTTGGATCCTATTCTTGTACATGCAACCCTGGTTTTTACCCTCAATGAGGATGG
AAGGTCTTGCCAAGATGTGAACGAGTGTGCCACCGAGAACCCTGCGTGCAAACCTGCGTCA
ACACCTACGGCTCTCTCATCTGCCGCTGTGACCCAGGATATGAACCTTGAGGAAGATGGCGTT
CATTGCAGTGATATGGACGAGTGCAGCTTCTCTGAGTTCCCTCTGCCAACATGAGTGTGTGAA
CCAGCCCGGCACATACTTCTGCTCCTGCCCTCCAGGCTACATCCTGCTGGATGACAACCGAA
GCTGCCAAGACATCAACGAATGTGAGCACAGGAACCACACGTGCAACCTGCAGCAGACGTGC
TACAATTTACAAGGGGGGCTTCAAATGCATCGACCCCATCCGCTGTGAGGAGCCTTATCTGAG
GATCAGTGATAACCGCTGTATGTGTCTGCTGAGAACCCTGGCTGCAGAGACCAGCCCTTTA
CCATCTTGTACCGGGACATGGACGTGGTGTGACGAGCTCCGTTCCCGCTGACATCTTCCAA
ATGCAAGCCACGACCCGCTACCCTGGGGCCTATTACATTTTCCAGATCAAATCTGGGAATGA
GGGAGAGAAATTTTACATGCGGCAAACGGGGCCCATCAGTGCCACCCTGGTGATGACACGCC
CCATCAAAGGGGCCCCGGGAAATCCAGCTGGACTTGGAATGATCACTGTCAACACTGTCTATC
AACTTCAGAGGCAGCTCCGTGATCCGACTGCGGATATATGTGTGCGCAGTACCCATTCTGAGC
CTCGGGCTGGAGCCTCCGACGCTGCCTCTCATTGGCACCAAGGGACAGGAGAAGAGAGGAAA
TAACAGAGAGAATGAGAGCGACACAGACGTTAGGCATTTCTCTGCTGAACGTTTCCCCGAAGA
GTCAGCCCCGACTTCCTGACTCTCACCTGTACTATTGCAGACCTGTCACCCTGCAGGACTTG
CCACCCCCAGTTCTTATGACACAGTTATCAAAAAGTATTATCATTGCTCCCCTGATAGAAGA
TTGTTGGTGAATTTTCAAGGCCTTCAGTTTATTTCCACTATTTTCAAAGAAAATAGATTAGG
TTTGCGGGGGTCTGAGTCTATGTTCAAAGACTGTGAACAGCTTGCTGTCACTTCTTCACCTC
TTCCACTCCTTCTCTCACTGTGTTACTGCTTTGCAAAGACCCGGGAGCTGGCGGGGAACCCT
GGGAGTAGCTAGTTTGGCTTTTGGCGTACACAGAGAAGGCTATGTAAACAAACCACAGCAGGA
TCGAAGGGTTTTTAGAGAATGTGTTTCAAACCATGCCTGGTATTTTCAACCATAAAAGAAG
TTTCAGTTGTCTTAAATTTGTATAACGGTTTAAATTTCTGTCTTGTTCATTTTGAAGTATTTT
AAAAAATATGTCGTAGAATTCCTTCGAAAGGCCTTCAGACACATGCTATGTTCTGTCTTCCC
AAACCCAGTCTCCTCTCCATTTTAGCCAGTGTTTTCTTTGAGGACCCCTTAATCTTGCTTT
CTTTAGAATTTTACCCAATTGGATTGGAATGCAGAGGTCTCCAACTGATTAAATATTTGA
AGAGA

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FIGURE 10

MPGIKRILTVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQ
NGGYLCIPRTNPVYRGYPYSNPYSTPYSGPYPAAAPPLSAPNYPTISRPLICRFGYQMDESNQ
CVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQLCANVPG
SYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSLICRCDPGYELEEDGVHCSDM
DECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQG
GFKCIDPIRCEEPLYLRISDNRCMCPAENPGCRDQPFITILYRDMDVVSGRSVPADIFQMATT
RYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEMITVNTVINFRGS
SVIRLRIYVSQYPF

Important features of the protein:

Signal peptide:

amino acids 1-25

N-glycosylation sites.

amino acids 283-287, 296-300

N-myristoylation sites.

amino acids 21-27, 64-70, 149-155, 186-192, 226-232, 242-248,
267-273, 310-316

Aspartic acid and asparagine hydroxylation sites.

amino acids 144-156, 181-193, 262-274

Cell attachment sequence.

amino acids 54-57

Calcium-binding EGF-like.

amino acids 131-166, 172-205, 211-245, 251-286

FIGURE 11

CAGGTCCAACCTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTC
GACCTCGACCCACGCGTCCGAACACAGGTCTTGTGCTGCAGAGAAGCAGTTGTTTTGCTG
GAAGGAGGGAGTGC GCGGGCTGCCCGGGCTCCTCCCTGCCGCCTCCTCTCAGTGGATGGTT
CCAGGCACCCTGTCTGGGGCAGGGAGGGCACAGGCCTGCACATCGAAGGTGGGGTGGGACCA
GGCTGCCCCCTCGCCCCAGCATCCAAGTCTCCTTGGGCGCCCGTGGCCCTGCAGACTCTCA
GGGCTAAGGTCTCTGTTGCTTTTTGGTTCCACCTTAGAAGAGGCTCCGCTTGACTAAGAGT
AGCTTGAAGGAGGCACC**ATGC**AGGAGCTGCATCTGCTCTGGTGGGCGCTTCTCCTGGGCCTG
GCTCAGGCCTGCCCTGAGCCCTGCGACTGTGGGGAAAAGTATGGCTTCCAGATCGCCGACTG
TGCCTACCGCGACCTAGAATCCGTGCCGCCTGGCTTCCCGGCCAATGTGACTACACTGAGCC
TGTCAGCCAACCGGCTGCCAGGCTTGCCGGAGGGTGCCTTCAGGGAGGTGCCCTGCTGCAG
TCGCTGTGGCTGGCACACAATGAGATCCGCACGGTGGCCGCCGGAGCCCTGGCCTCTCTGAG
CCATCTCAAGAGCCTGGACCTCAGCCACAATCTCATCTCTGACTTTGCCTGGAGCGACCTGC
ACAACCTCAGTGCCCTCCAATTGCTCAAGATGGACAGCAACGAGCTGACCTTCATCCCCCGC
GACGCCTTCCGCAGCCTCCGTGCTCTGCGCTCGCTGCAACTCAACCACAACCGCTTGCACAC
ATTGGCCGAGGGCACCTTCACCCCGCTCACCGCGCTGTCCACCTGCAGATCAACGAGAACC
CCTTCGACTGCACCTGCGGCATCGTGTGGCTCAAGACATGGGCCCTGACCACGGCCGTGTCC
ATCCCGGAGCAGGACAACATCGCCTGCACCTCACCCCATGTGCTCAAGGGTACACCGCTGAG
CCGCCTGCCGCCACTGCCATGCTCGGCGCCCTCAGTGCAGCTCAGCTACCAACCCAGCCAGG
ATGGTGCCGAGCTGCGGCCTGGTTTTGTGCTGGCACTGCACTGTGATGTGGACGGGCAGCCG
GCCCCCTCAGCTTCACTGGCACATCCAGATAACCCAGTGGCATTGTGGAGATCACCAGCCCCAA
CGTGGGCACTGATGGGCGTGCCCTGCCTGGCACCCCTGTGGCCAGCTCCCAGCCGCGCTTCC
AGGCCTTTGCCAATGGCAGCCTGCTTATCCCCGACTTTGGCAAGCTGGAGGAAGGCACCTAC
AGCTGCCTGGCCACCAATGAGCTGGGCAGTGTGAGAGCTCAGTGGACGTGGCACTGGCCAC
GCCCCGTGAGGGTGGTGAGGACACACTGGGGCGCAGGTTCATGGCAAAGCGGTTGAGGGGAA
AGGGCTGCTATACGGTTGACAACGAGGTGCAGCCATCAGGGCCGGAGGACAATGTGGTCATC
ATCTACCTCAGCCGTGCTGGGAACCCTGAGGCTGCAGTCGCAGAAGGGGTCCCTGGGCAGCT
GCCCCCAGGCCTGCTCCTGCTGGGCCAAAGCCTCCTCCTTCTTCTCCTCACCTCCTTCT**T**
AGCCCCACCCAGGGCTTCCCTAACTCCTCCCCCTTGCCCCCTACCAATGCCCTTTAAGTGCTG
CAGGGGTCTGGGGTTGGCAACTCCTGAGGCCTGCATGGGTGACTTCACATTTTCTCCTACCTCT
CCTTCTAATCTCTTCTAGAGCACCTGCTATCCCCAACTTCTAGACCTGCTCCAAACTAGTGA
CTAGGATAGAATTTGATCCCCTAACCTCACTGTCTGCGGTGCTCATTGCTGCTAACAGCATTG
CCTGTGCTCTCCTCTCAGGGGCAGCATGCTAACGGGGCGACGTCCTAATCCAACCTGGGAGAA
GCCTCAGTGGTGGAATTCCAGGCACTGTGACTGTCAAGCTGGCAAGGGGCCAGGATTGGGGGA
ATGGAGCTGGGGCTTAGCTGGGAGGTGGTCTGAAGCAGACAGGGAATGGGAGAGGAGGATGG
GAAGTAGACAGTGGCTGGTATGGCTCTGAGGCTCCCTGGGGCCTGCTCAAGCTCCTCCTGCT
CCTTGCTGTTTTCTGATGATTTGGGGGCTTGGGAGTCCCTTTGTCTCATCTGAGACTGAAA
TGTGGGGATCCAGGATGGCCTTCCTTCTTACCCTTCTCCCTCAGCCTGCAACCTCTAT
CCTGGAACCTGTCCTCCCTTTCTCCCCAACTATGCATCTGTTGTCTGCTCCTCTGCAAAGGC
CAGCCAGCTTGGGAGCAGCAGAGAAATAAACAGCATTTCTGATGCCAAAAAAAAAAAAAAAAA
AAGGGCGGCCGCGACTCTAGAGTCGACCT

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FIGURE 12

MQELHLLWWALLLGLAQACPEPCDCGEKYGFQIADCAYRDLESVPPGFANVTTLSSLNRL
PGLPEGAFFREVPLLQSLWLAHNEIRTVAAGALASLSHLKSLDLSHNLISDFAWSDLHNLSAL
QLLKMDSNELTFIPRDAFRSLRALRSLQLNHNRLHTLAEGTFTPLTALSHLQINENPFDCCTC
GIVWLKTTWALTAVSIPEDNIACTSPHVLKGTPLSRLPPLPCSAPSVQLSYQPSQDGAELR
PGFVLALHCDVDGQPAPQLHWHIQIPSGIVEITSPNVGTDGRALPGTPVASSQPRFQAFANG
SLLIPDFGKLEEGTYSCLATNELGSAESSVDVALATPGEGGEDTLGRRFHGKAVEGKGCYTV
DNEVQPSGPEDNVVIYLSRAGNPEAAVAEGVPGQLPPGLLLLQSLLLFFFLTSF

Important features of the protein:

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 403-418

N-glycosylation sites.

amino acids 51-55, 120-124, 309-313

Tyrosine kinase phosphorylation site.

amino acids 319-326

N-myristoylation sites.

amino acids 14-20, 64-70, 92-98, 218-224, 294-300, 323-329,
334-340, 350-356, 394-400

Amidation site.

amino acids 355-359

Leucine rich repeats.

amino acids 51-74, 75-98, 99-122, 123-146, 147-170

Leucine rich repeat C-terminal domain.

amino acids 180-230

FIGURE 13

CCAGGCCGGGAGGCGACGCGCCCGAGCCGTCTAAACGGGAACAGCCCTGGCTGAGGGAGCTGC
AGCGCAGCAGAGTATCTGACGGCGCCAGGTTGCGTAGGTGCGGCACGAGGAGTTTTCCCGGC
AGCGAGGAGGTCCTGAGCAGCATGGCCCCGGAGGAGCGCCTTCCCTGCCGCCGCGCTCTGGCT
CTGGAGCATCCTCCTGTGCCTGCTGGCACTGCGGGCGGAGGCCGGGCGCCGCAGGAGGAGA
GCCTGTACCTATGGATCGATGCTCACCAGGCAAGAGTACTCATAGGATTTGAAGAAGATATC
CTGATTGTTTCAGAGGGGAAAATGGCACCTTTTACACATGATTTAGAAAAGCGCAACAGAG
AATGCCAGCTATTCTGTCAATATCCATTCCATGAATTTTACCTGGCAAGCTGCAGGGCAGG
CAGAATACTTCTATGAATTCCTGTCCTTGCCTCCCTGGATAAAGGCATCATGGCAGATCCA
ACCGTCAATGTCCCTCTGCTGGGAACAGTGCCTCACAAGGCATCAGTTGTTCAAGTTGGTTT
CCCATGTCTTGGAAAACAGGATGGGGTGGCAGCATTTGAAGTGGATGTGATTGTTATGAATT
CTGAAGGCAACACCATTTCTCCAAACACCTCAAAATGCTATCTTCTTTAAACATGTCAACAA
GCTGAGTGCCCGAGGCGGGTGCCGAAATGGAGGCTTTTGTAATGAAAGACGCATCTGCGAGTG
TCCTGATGGGTTCCACGGACCTCACTGTGAGAAAGCCCTTTGTACCCACGATGTATGAATG
GTGGACTTTGTGTGACTCCTGGTTTCTGCATCTGCCACCTGGATTCTATGGAGTGAAGTGT
GACAAAGCAAACCTGCTCAACCACCTGCTTTAATGGAGGGACCTGTTTCTACCTGGAAAATG
TATTTGCCCTCCAGGACTAGAGGGAGAGCAGTGTGAAATCAGCAAATGCCACAACCCTGTC
GAAATGGAGGTAAATGCATTGGTAAAAGCAAATGTAAGTGTTCCAAAGGTTACCAGGGAGAC
CTCTGTTCAAAGCCTGTCTGCGAGCCTGGCTGTGGTGCACATGGAACCTGCCATGAACCCAA
CAAATGCCAATGTCAAGAAGGTTGGCATGGAAGACACTGCAATAAAAGGTACGAAGCCAGCC
TCATACATGCCCTGAGGCCAGCAGGCGCCAGCTCAGGCAGCACACGCCTTCACTTAAAAAG
GCCGAGGAGCGGCGGGATCCACCTGAATCCAATTACATCTGGTGAACTCCGACATCTGAAAC
GTTTTAAGTTACACCAAGTTCATAGCCTTTGTTAACCTTTTCATGTGTTGAATGTTCAAATAA
TGTTCAATTACACTTAAGAATACTGGCCTGAATTTTATTAGCTTCATTATAAATCACTGAGCT
GATATTTACTCTTCCTTTTAAGTTTTCTAAGTACGTCTGTAGCATGATGGTATAGATTTTCT
TGTTTCAGTGCTTTGGGACAGATTTTATATTATGTCAATTGATCAGGTAAAAATTTTCAGTG
TGTAAGTTGGCAGATATTTTCAAATTTACAATGCATTTATGGTGTCTGGGGGCAGGGGAACAT
CAGAAAGGTTAAATTGGGCAAAAATGCGTAAGTCACAAGAATTTGGATGGTGCAGTTAATGT
TGAAGTTACAGCATTTTCAGATTTTATTGTCAGATATTTAGATGTTTGTTACATTTTTTAAAAA
TTGCTCTTAATTTTTTAACTCTCAATACAATATATTTTGACCTTACCATTATTCCAGAGATT
CAGTATTAATAAAAAAAAAAATTACACTGTGGTAGTGGCATTTAACAATATAATATATTCTA
AACACAATGAAATAGGGAATATAATGTATGAACTTTTTGCATTGGCTTGAAGCAATATAATA
TATTGTAAACAAAACACAGCTCTTACCTAATAAACATTTTATACTGTTTGTATGTATAAAAT
AAAGGTGCTGCTTTAGTTTTTTGGAAAAAATAAAAAAAAAAAAAAAAAA

FIGURE 14

MARRSAFPAAALWLWSILLCLLALRAEAGPPQEESLYLWIDAHQARVLIGFEEDILIVSEGK
 MAPFTHDFERKAQQRMIPAIPVNIHSMNFTWQAAGQAEYFYEFSLRSLDKGIMADPTVNVPLL
 GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPPGGC
 RGGGFCNERRICECPDGFHGHCEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCST
 TCFNGGTCTFYPGKCICPPGLEGEQCEISKCPQPCRNGGKCIGKSKCKCSKGYQGDLCSPVC
 EPGCGAHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAEERRDP
 PESNYIW

Signal sequence.

amino acids 1-28

N-glycosylation sites.

amino acids 88-92, 245-249

Tyrosine kinase phosphorylation site.

amino acids 370-378

N-myristoylation sites.

amino acids 184-190, 185-191, 189-195, 315-321

ATP/GTP-binding site motif A (P-loop).

amino acids 285-293

EGF-like domain cysteine pattern signature.

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

FIGURE 15

AGAACCTCAGAAATGTGAGTTATTTGGGAATGGCTGTTTGTAATGTCCTTACGTAAGCCAA
GAGGAGGTCTTGACTTGGGGTCCCAGGGGTACCGCAGATCCCAGGGACTGGAGCAGCACTAG
CAAGCTCTGGAGGATGAGCCAGGAGTCTGGAATTGAGGCTGAGCCAAAGACCCCAGGGCCGT
CTCAGTCTCATAAAAGGGGATCAGGCAGGAGGAGTTTGGGAGAAACCTGAGAAGGGCCTGAT
TTGCAGCATCATGATGGGCCTCTCCTTGGCCTCTGCTGTGCTCCTGGCCTCCCTCCTGAGTC
TCCACCTTGGAAGTGCCACACGTGGGAGTGACATATCCAAGACCTGCTGCTTCCAATACAGC
CACAAGCCCCTTCCCTGGACCTGGGTGCGAAGCTATGAATTCACCAGTAACAGCTGCTCCCA
GCGGGCTGTGATATTCACCTACCAAAGAGGCAAGAAAGTCTGTACCCATCCAAGGAAAAAAT
GGGTGCAAAAATACATTTCTTTACTGAAAACCTCCGAAACAATTGTGACTCAGCTGAATTTTC
ATCCGAGGACGCTTGGACCCCGCTCTTGGCTCTGCAGCCCTCTGGGGAGCCTGCGGAATCTT
TTCTGAAGGCTACATGGACCCCGCTGGGGAGGAGAGGGTGTTTCCTCCCAGAGTTACTTTAAT
AAAGGTTGTTCATAGAGTTGAAA
AAA

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FIGURE 16

MMGLSLASAVLLASLLSLHLGTATRGSDISKTCCEFQYSHKPLPWTWVRSYEFTSNSCSQRAV
IFTTKRGKKVCTHPRKKWVQKYISLLKTPKQL

Important features of the protein:

Signal peptide:

amino acids 1-23

N-myristoylation sites.

amino acids 3-9, 26-32

Amidation site.

amino acids 68-72

Small cytokines (intecrine/chemokine).

amino acids 23-88

FIGURE 17

GCGAGAACCTTTGCACGCGCACAACTACGGGGACGATTTCTGATTGATTTTTGGCGCTTTCGATCCACCCTCC
TCCCTTCTC**ATG**GGGACTTTGGGGACAAAGCGTCCCGACCGCCTCGAGCGCTCGAGCAGGGCGCTATCCAGGAGC
CAGGACAGCGTCGGGAACCAGACCATGGCTCCTGGACCCCAAGATCCTTAAGTTCGTCTTTCATCGTCGCGG
TTCTGCTGCCGGTCCGGGTTGACTCTGCCACCATCCCCCGCAGGACGAAGTTCCCCAGCAGACAGTGGCCCCA
CAGCAACAGAGGGCGCAGCCTCAAGGAGGAGGAGTGTCCAGCAGGATCTCATAGATCAGAATACTGGAGCCTG
TAACCCGTGCACAGAGGGTGTGGATTACACCATTGCTTCCAACAATTTGCCTTCTTGCTGCTATGTACAGTTT
GTAATCAGGTCAAACAATAAAAGTTCCTGTACCACGACCAGAGACACCGTGTGTGCTAGTGTGAAAAAGGAAGC
TTCAGGATAAAAACTCCCTGAGATGTGCCGGACGTGTAGAACAGGGTGTCCAGAGGGATGGTCAAGGTGAG
TAATTGTACGCCCCGGAGTGACATCAAGTGCAAAAATGAATCAGCTGCCAGTTCCACTGGGAAAACCCAGCAG
CGGAGGAGACAGTGACCACCATCCTGGGGATGCTTGCTCTCCCTATCACTACCTTATCATCATAGTGGTTTTTA
GTCATCATTTTTAGCTGTGGTTGTGGTTGGCTTTTCATGTGCGGAAGAAATTCATTTCTTACCTCAAAGGCATCTG
CTCAGGTGGTGGAGGAGGTCCCGAACGTGTGCACAGAGTCTTTTTCCGGCGGCGTTCATGTCCTTCACGAGTTC
CTGGGGCGGAGGACAATGCCCGCAACGAGACCCTGAGTAACAGATACTTGCAGCCCACCCAGGTCTCTGAGCAG
GAAATCCAAGGTGAGGAGCTGGCAGAGCTAACAGGTGTGACTGTAGAGTCGCCAGAGGAGCCACAGCGTCTGCT
GGAACAGGCAGAAGCTGAAGGGTGTGAGAGGAGGAGGCTGCTGGTTCCAGTGAATGACGCTGACTCCGCTGACA
TCAGCACCTTGCTGGATGCCTCGGCAACACTGGAAGAAGGACATGCAAAGGAAACAATTCAGGACCAACTGGTG
GGCTCCGAAAAGCTCTTTTATGAAGAAGATGAGGCAGGCTCTGCTACGTCCTGCCTG**TGA**AAGAATCTCTTCAG
GAAACCAGAGCTTCCCTCATTACCTTTTCTCCTACAAAGGGAAGCAGCCTGGAAGAAACAGTCCAGTACTTGA
CCCATGCCCCAACAACTCTACTATCCAATATGGGGCAGCTTACCAATGGTCTAGAACTTTGTAAACGCACTT
GGAGTAATTTTTATGAAATACTGCGTGTGATAAGCAAACGGGAGAAATTTATATCAGATTCTTGCTGCTAGAT
TATACGATTGTGTATTAAGGGTCTGTTTAGGCCACATGCGGTGGCTCATGCCTGTAATCCCAGCACTTTGATAG
GCTGAGGCAGGTGGATTGCTTGAGCTCGGGAGTTGAGACCAGCCTCATCAACACAGTGAAACTCCATCTCAAT
TTAAAAAGAAAAAAAGTGGTTTTAGGATGTCATTCTTTGCAGTTCTTCATCATGAGACAAGTCTTTTTTTCTGC
TTCTTATATTGCAAGCTCCATCTCTACTGGTGTGTGCATTAAATGACATCTAACTACAGATGCCGCACAGCCAC
AATGCTTTGCCTTATAGTTTTTTAACTTTAGAACGGGATTATCTTGTTATTACCTGTATTTTCAGTTTCGGATA
TTTTTGACTTAATGATGAGATTATCAAGACGTAGCCCTATGCTAAGTCATGAGCATATGGACTTACGAGGGTTC
GACTTAGAGTTTTGAGCTTTAAGATAGGATTATTGGGGCTTACCCCCACCTTAATTAGAGAAACATTTATATTG
CTTACTACTGTAGGCTGTACATCTCTTTCCGATTTTTGTATAATGATGTAAACATGGAAAACTTTAGGAAAT
GCACTTATTAGGCTGTTTACATGGGTGCTGGATACAAATCAGCAGTCAAAAAAGACTAAAAATATAACTAGT
GACGGAGGGAGAAATCCTCCCTCTGTGGGAGGCACCTTACGATTCAGATTCCAGTTCTCCCTCGCGCCCTGAGACTG
GACCAGGGTTTGATGGCTGGCAGCTTCTCAAGGGGCAGCTTGTCTTACTTGTAAATTTTAGAGGTATATAGCCA
TATTTATTTATAAATAAATATTTATTTATTTATTTATAAGTAGATGTTTACATATGCCAGGATTTTGAAGAGC
CTGGTATCTTTGGGAAGCCATGTGTCTGGTTTTGTCGTGCTGGGACAGTCATGGGACTGCATCTTCCGACTTGTC
CACAGCAGATGAGGACAGTGAGAATTAAGTTAGATCCGAGACTGCGAAGAGCTTCTCTTTCAAGCGCCATTACA
GTTGAACGTTAGTGAATCTTGAGCCTCATTTGGGCTCAGGGCAGAGCAGGTGTTTATCTGCCCCGGCATCTGCC
ATGGCATCAAGAGGGAAGAGTGGACGGTCTTGGGAATGGTGTGAAATGGTTGCCGACTCAGGCATGGATGGGC
CCCTCTCGCTTCTGGTGGTCTGTGAACTGAGTCCCTGGGATGCCTTTTAGGGCAGAGATTCCTGAGCTGCGTTT
TAGGGTACAGATTCCCTGTTTGAGGAGCTTGGCCCCCTCTGTAAGCATCTGACTCATCTCAGAGATATCAATTCT
TAAACACTGTGACAACGGGATCTAAATGGCTGACACATTTGTCTTGTGTACGTTCCATTATTTTATTTAAA
AACCTCAGTAATCGTTTTAGCTTCTTTCCAGCAAACCTCTTCCACAGTAGCCAGTCTGGTAGGATAAATTA
CGGATATAGTCATTCTAGGGGTTTCAGTCTTTTCCATCTCAAGGCATTGTGTGTTTTGTTCCGGGACTGGTTTG
GCTGGGACAAAGTTAGAACTGCCTGAAGTTCCGCACATTGAGATTGTTGTGTCCATGGAGTTTTAGGAGGGGATG
GCCTTTCCGGTCTTCGCACTTCCATCCTCTCCCACTTCCATCTGGCGTCCCACACCTTGTCCCCTGCACTTCTG
GATGACACAGGGTGTGCTGCCTCCTAGTCTTTGCCTTTGCTGGGCTTCTGTGCAGGAGACTTGGTCTCAAAG
CTCAGAGAGAGCCAGTCCGGTCCCAGCTCCTTTGTCCCTTCTCAGAGGCCTTCTTGAAGATGCATCTAGACT
ACCAGCCTTATCAGTGTTTAAGCTTATTCCTTTAACATAAGCTTCTGACAACATGAAATTGTTGGGGTTTTTT
GGCGTTGGTTGATTTGTTTAGGTTTTGCTTTATACCCGGGCCAAATAGCACATAACACCTGGTTATATATGAAA
TACTCATATGTTTATGACCAAAATAAATATGAAACCTCATRTAAAAA

FIGURE 18

MGLWGQSVPTASSARAGRYPGARTASGTRPWLLDPKILKFVVFIVAVLLPVRVDSATIPRQD
EVPQQTVAPQQQRRSLKEEECPAGSHRSEYTGACNPCTEGVDYTIASNNLPSCLLCTVCKSG
QTNKSSCTTTTRDTVCQCEKGSFQDKNSPEMCRTCRTGCPRGMVKVSNCTPRSDIKCKNESAA
SSTGKTPAAEETVTTILGMLASPYHYLIIIVVLVIIILAVVVVGFSCRKKFISYLKGICSGGG
GGPERVHRVLFRRRSCPSRVPGAEDNARNETLSNRYLQPTQVSEQEIQGQELAEELTGVTVES
PEEPQRLLEQAEAEGCQRRRLVFPVNDADSADISTLLDASATLEEGHAKETIQDQLVGSEKL
FYEEDEAGSATSCCL

Important features of the protein:

Transmembrane domains:

amino acids 35-52, 208-230

N-glycosylation sites.

amino acids 127-131, 182-186, 277-281

Glycosaminoglycan attachment site.

amino acids 245-249

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 260-264

N-myristoylation sites.

amino acids 21-27, 86-92, 102-108, 161-167, 242-248, 270-276,
297-303, 380-386

ATP/GTP-binding site motif A (P-loop).

amino acids 185-193

TNFR/NGFR cysteine-rich region.

amino acids 99-139

FIGURE 19

GCGGCACCTGGAAG**ATG**CGCCCATTGGCTGGTGGCCTGCTCAAGGTGGTGTTCGTGGTCTTC
GCCTCCTTGTGTGCCTGGTATTCGGGGTACCTGCTCGCAGAGCTCATTCCAGATGCACCCCT
GTCCAGTGCTGCCATATAGCATCCGCAGCATCGGGGAGAGGCCTGTCCTCAAAGCTCCAGTCC
CCAAAAGGCAAAAATGTGACCACTGGACTCCCTGCCCATCTGACACCTATGCCTACAGGTTA
CTCAGCGGAGGTGGCAGAAGCAAGTACGCCAAAATCTGCTTTGAGGATAACCTACTTATGGG
AGAACAGCTGGGAAATGTTGCCAGAGGAATAAACATTGCCATTGTCAACTATGTAAGTGGGA
ATGTGACAGCAACACGATGTTTTGATATGTATGAAGGCGATAACTCTGGACCGATGACAAAG
TTTATTCAGAGTGCTGCTCCAAAATCCCTGCTCTTCATGGTGACCTATGACGACGGAAGCAC
AAGACTGAATAACGATGCCAAGAATGCCATAGAAGCACTTGGAAGTAAAGAAATCAGGAACA
TGAAATTCAGGTCTAGCTGGGTATTTATTGCAGCAAAAGGCTTGGAACCTCCCTTCCGAAATT
CAGAGAGAAAAGATCAACCACTCTGATGCTAAGAACAACAGATATTCTGGCTGGCCTGCAGA
GATCCAGATAGAAGGCTGCATACCCAAAGAACGAAGC**TGA**CACTGCAGGGTCCTGAGTAAAT
GTGTTCTGTATAAAACAAATGCAGCTGGAATCGCTCAAGAATCTTATTTTTCTAAATCCAACA
GCCCATATTTGATGAGTATTTTGGGTTTGTTGTAAACCAATGAACATTTGCTAGTTGTATCA
AATCTTGGTACGCAGTATTTTTATACCAGTATTTTATGTAGTGAAGATGTCAATTAGCAGGA
AACTAAAATGAATGGAAATTCTTAAAAA

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FIGURE 20

MRPLAGGLLKVVVFVVFASLCAWYSGYLLAELIPDAPLSSAAYSIRSIGERPVLKAPVPKRQK
CDHWTPCPSDTYAYRLLSGGGRSKYAKICFEDNLLMGEQLGNVARGINIAIVNYVTGNVTAT
RCFDMYEGDNSGPMTKFIQSAAPKSLLFMVTYDDGSTRLNNDKNAIEALGSKEIRNMKFRS
SWVFIAAKGLELPSEIQREKINHSDAKNNRYSGWPAEIQIEGCIPKERS

Important features of the protein:

Signal peptide:

amino acids 1-20

N-glycosylation sites.

amino acids 120-124, 208-212

Glycosaminoglycan attachment site.

amino acids 80-84

N-myristoylation sites.

amino acids 81-87, 108-114, 119-125

FIGURE 21

CCGGGGAGGGGAGGGCCCGTCCCGCCCCCTCCCCGTCTCTCCCCGCCCCCTCCCCGTCCCTCCC
GCCGAAGCTCCGTCCCGCCCCGCGGGCCGGCTCCGCCCTCACCTCCCGGCCGCGGCTGCCCTC
TGCCCGGGTTGTCCAAG**ATG**GAGGGCGCTCCACCGGGGTCGCTCGCCCTCCGGCTCCTGCTG
TTCGTGGCGCTACCCGCCTCCGGCTGGCTGACGACGGGGCGCCCCCGAGCCGCCGCCGCTGTC
CGGAGCCCCACAGGACGGCATCAGAATTAATGTAAC TACACTGAAAGATGATGGGGACATAT
CTAAACAGCAGGTTGTTCTTAACATAACCTATGAGAGTGGACAGGTGTATGTAAATGACTTA
CCTGTAAATAGTGGTGTAAACCCGAATAAGCTGTCAGACTTTGATAGTGAAGAATGAAAATCT
TGAAAATTTGGAGGAAAAAGAATATTTTGG AATTGTCAGTGTAAGGATTTTAGTTCATGAGT
GGCCTATGACATCTGGTTCCAGTTTGCAACTAATTGTCATTCAAGAAGAGGTAGTAGAGATT
GATGGAAAACAAGTTCAGCAAAAGGATGTCACTGAAATTGATATTTTAGTTAAGAACCGGGG
AGTACTCAGACATTCAAAC TATAACCCTCCCTTTGGAAGAAAGCATGCTCTACTCTATTTCTC
GAGACAGTGACATTTTATTTACCCTTCCTAACCTCTCCAAAAAAGAAAGTGTTAGTTCACTG
CAAACCACTAGCCAGTATCTTATCAGGAATGTGGAAACCACTGTAGATGAAGATGTTTTACC
TGGCAAGTTACCTGAAACTCCTCTCAGAGCAGAGCCGCCATCTTCATATAAGGTAATGTGTC
AGTGGATGGAAAAGTTTAGAAAAGATCTGTGTAGGTTCTGGAGCAACGTTTTTCCCAGTATTC
TTTCAGTTTTTTGAACATCATGGTGGTTGGAATTACAGGAGCAGCTGTGGTAATAACCATCTT
AAAGGTGTTTTTCCCAGTTTCTGAATACAAAGGAATTCCTCAGTTGGATAAAGTGGACGTCA
TACCTGTGACAGCTATCAACTTATATCCAGATGGTCCAGAGAAAAGAGCTGAAAACCTTGAA
GATAAAACATGTATT**TAA**AACGCCATCTCATATCATGGACTCCGAAGTAGCCTGTTGCCTCC
AAATTTGCCACTTGAATATAATTTTCTTTAAATCGTT

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FIGURE 22

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60783
><subunit 1 of 1, 330 aa, 1 stop
><MW: 36840, pI: 4.84, NX(S/T): 4
MEGAPPGSLALRLLLFVALPASGWLTGGAPEPPPLSGAPQDGIRINVTTLKDDGDISKQQVV
LNITYESGQVYVNDLPVNSGVTRISCQTLIVKNENLENLEEKEYFGIVSVRILVHEWPMTSG
SSLQLIVIQEEVVEIDGKQVQKQDVTEIDILVKNRGVLRHSNYTLPLEESMLYSISRDSIL
FTLPNLSKKESVSSLQTTSQYLIRNVETTVDLPGKLPETPLRAEPPSSYKVMCQWMEKF
RKDLCRFWSNVFPVFFQFLNIMVVGITGAADVITILKVFFPVSEYKGILQLDKVDVIPVTAI
NLYPDGPKEKRAENLEDKTCI
```

Important features of the protein:

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 266-284

Leucine zipper pattern.

amino acids 155-176

N-glycosylation sites.

amino acids 46-49, 64-67, 166-169, 191-194

FIGURE 23

CGTCTCTGCGTTTCGCC**ATG**CGTCCCGGGGCGCCAGGGCCACTCTGGCCTCTGCCCTGGGGGG
CCCTGGCTTGGGCGGTGGGCTTCGTGAGCTCCATGGGCTCGGGGAACCCCGCGCCCGGTGGT
GTTTGCTGGCTCCAGCAGGGCCAGGAGGCCACCTGCAGCCTGGTGCTCCAGACTGATGTCAC
CCGGGCCGAGTGCTGTGCCTCCGGCAACATTGACACCGCCTGGTCCAACCTCACCCACCCGG
GGAACAAGATCAACCTCCTCGGCTTCTTGGGCTTGTCCACTGCCTTCCCTGCAAAGATTCTG
TGCGACGGCGTGGAGTGCGGCCCCGGGCAAGGCGTGCCGCATGCTGGGGGGCGCCCGCGCTG
CGAGTGCGCGCCCCGACTGCTCGGGGCTCCCGGCGCGGCTGCAGGTCTGCGGCTCAGACGGCG
CCACCTACCGCGACGAGTGCGAGCTGCGCGCCGCGCGCTGCCGCGGCCACCCGGACCTGAGC
GTCATGTACCGGGGCGCTGCCGCAAGTCTGTGAGCACGTGGTGTGCCCGCGGCCACAGTC
GTGCGTCGTGGACCAGACGGGCAGCGCCCACTGCGTGGTGTGTGCGAGCGGCGCCCTGCCCTG
TGCCCTCCAGCCCCGGCCAGGAGCTTTGCGGCAACAACAACGTACCTACATCTCCTCGTGC
CACATGCGCCAGGCCACCTGCTTCCCTGGGCGCTCCATCGGCGTGCGCCACGCGGGCAGCTG
CGCAGGCACCCCTGAGGAGCCGCCAGGTGGTGAGTCTGCAGAAGAGGAAGAGAACTTCGTG**T**
GAGCCTGCAGGACAGGCCTGGGCTGGTGCCCCGAGGCCCCCATCATCCCTGTATTATTTATT
GCCACAGCAGAGTCTAATTTATATGCCACGGACACTCCTTAGAGCCCGGATTCGGACCACTT
GGGGATCCCAGAACCTCCCTGACGATATCCTGGAAGGACTGAGGAAGGGAGGCCTGGGGGCC
GGCTGGTGGGTGGGATAGACCTGCGTTCCGGACACTGAGCGCCTGATTTAGGGCCCTTCTCT
AGGATGCCCCAGCCCCCTACCCTAAGACCTATTGCCGGGGAGGATTCCACACTTCCGCTCCTT
TGGGGATAAACCTATTAATTATTGCTACTATCAAGAGGGCTGGGCATTCTCTGCTGGTAATT
CCTGAAGAGGCATGACTGCTTTTCTCAGCCCCAAGCCTCTAGTCTGGGTGTGTACGGAGGGT
CTAGCCTGGGTGTGTACGGAGGGTCTAGCCTGGGTGAGTACGGAGGGTCTAGCCTGGGTGAG
TACGGAGGGTCTAGCCTGGGTGAGTACGGAGGGTCTAGCCTGGGTGTGTATGGAGGATCTAG
CCTGGGTGAGTATGGAGGGTCTAGCCTGGGTGAGTATGGAGGGTCTAGCCTGGGTGTGTATG
GAGGGTCTAGCCTGGGTGAGTATGGAGGGTCTAGCCTGGGTGTGTATGGAGGGTCTAGCCTG
GGTGAGTATGGAGGGTCTAGCCTGGGTGTGTACGGAGGGTCTAGTCTGAGTGCGTGTGGGGA
CCTCAGAACACTGTGACCTTAGCCAGCAAGCCAGGCCCTTCATGAAGGCCAAGAAGGCTGC
CACCATTCCCTGCCAGCCCAAGAACTCCAGCTTCCCCACTGCCTCTGTGTGCCCTTTGCGT
CCTGTGAAGGCCATTGAGAAATGCCAGTGTGCCCCCTGGGAAAGGGCACGGCCTGTGCTCC
TGACACGGGCTGTGCTTGGCCACAGAACCACCCAGCGTCTCCCCTGCTGCTGTCCACGTCAG
TTCATGAGGCAACGTCGCGTGGTCTCAGACGTGGAGCAGCCAGCGGCAGCTCAGAGCAGGGC
ACTGTGTCCGGCGGAGCCAAGTCCACTCTGGGGGAGCTCTGGCGGGGACCACGGGCCACTGC
TCACCCACTGGCCCCGAGGGGGGTGTAGACGCCAAGACTCACGCATGTGTGACATCCGGAGT
CCTGGAGCCGGGTGTCCCAGTGGCACCACTAGGTGCCTGCTGCCTCCACAGTGGGGTTCACA
CCCAGGGCTCCTTGGTCCCCCACAACCTGCCCCGGCCAGGCCTGCAGACCCAGACTCCAGCC
AGACCTGCCTCACCCACCAATGCAGCCGGGGCTGGCGACACCAGCCAGGTGCTGGTCTTGGG
CCAGTTCTCCACGACGGCTCACCTCCCCTCCATCTGCGTTGATGCTCAGAATCGCCTACC
TGTGCCTGCGTGTAAACCACAGCCTCAGACCAGCTATGGGGAGAGGACAACACGGAGGATAT
CCAGCTTCCCCGGTCTGGGGTGAGGAATGTGGGGAGCTTGGGCATCCTCCTCCAGCCTCCTC
CAGCCCCCAGGCAGTGCCTTACCTGTGGTGCCAGAAAAGTGCCCTAGGTTGGTGGGTCTA
CAGGAGCCTCAGCCAGGCAGCCACCCACCCCTGGGGCCCTGCCTCACCAAGGAATAAAGA
CTCAAGCCATAAAAAAAA

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FIGURE 24

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62306

<subunit 1 of 1, 263 aa, 1 stop

<MW: 27663, pI: 6.77, NX(S/T): 2

MRPGAPGPLWPLPWGALAWAVGVSSMSGNPAPGGVCWLQQGQEATCSLVLQTDVTRA ECC
ASGNIDTAWSNLTHPGNKINLLGFLGLVHCLPCKDSCDGVCEGPGKACRMLGGRPRCECAPD
CSGLPARLQVCGSDGATYRDECELRAARCRGHPDLSVMYRGRCRKSCEHVVCPRPQSCVVDQ
TGSAHCVVCRAAPCPVPSSPGQELCGNNNVTYISSCHMRQATCFLGRSIGVRHAGSCAGTPE
EPPGGESAEEEEENFV

Important features:

Signal peptide:

amino acids 1-20

N-glycosylation sites.

amino acids 73-77, 215-219

Osteonectin domain proteins.

amino acids 97-130, 169-202

FIGURE 25

FIGURE 26

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62880

<subunit 1 of 1, 505 aa, 1 stop

<MW: 56640, pI: 6.10, NX(S/T): 4

MGRVVAELVSSLLGLWLLLCSCGCPEGAELRAPD KIAIIGAGIGGTSAAYYLRQKFGKDVK
IDLFEREEVGGRLATMMVQGGQEYEAGGSVIHPLNLHMKRFVKDLGLSAVQASGGLLGIYNGE
TLVFEE SNWFIINVIKLVWRYGFQSLRMHMWVEDVLDKFMRIYRYQSHDYAFSSVEKLLHAL
GGDDFLGMLNRTLLET LQKAGFSEKFLNEMIAPVMRVNYGQSTDINAFVGAVSLSCSDSGLW
AVEGGNKLVC SGLLQASKSNLISGSVMYIEEKT KTKYTGNPTKMYEVVYQIGTETRSDFYDI
VLVATPLNRKMSNITFLNFDPPIEEFHQYYQHIVTTLVKGELNTSIFSSRPIDKFG LNTVLT
TDNSDLFINSIGIVPSVREKEDPEPSTDGTYVWKIFSQETLT KAQILKLFLSYDYAVKKPWL
AYPHYKPPEKCP SIILHDRLYYLN GIECAASAMEMSAIAAHNAALLAYHRWNGHTDMIDQDG
LYEKLKTEL

Important features:**Signal peptide:**

amino acids 1-23

N-glycosylation sites.

amino acids 196-200, 323-327, 353-357

Tyrosine kinase phosphorylation site.

amino acids 291-298

N-myristoylation sites.

amino acids 23-29, 41-47, 43-49, 45-51, 46-52, 72-78, 115-121,
119-125, 260-266, 384-390, 459-465

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 12-23, 232-243

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FIGURE 27

CATTTCCAACAAGAGCACTGGCCAAGTCAGCTTCTTCTGAGAGAGTCTCTAGAAGAC**ATG**AT
GCTACACTCAGCTTTGGGTCTCTGCCTCTTACTCGTCACAGTTTCTTCCAACCTTGCCATTG
CAATAAAAAAGGAAAAGAGGCCTCCTCAGACACTCTCAAGAGGATGGGGAGATGACATCACT
TGGGTACAACTTATGAAGAAGGTCTCTTTTATGCTCAAAAAAGTAAGAAGCCATTAATGGT
TATTCATCACCTGGAGGATTGTCAATACTCTCAAGCACTAAAGAAAGTATTTGCCCAAATG
AAGAAATACAAGAAATGGCTCAGAATAAGTTCATCATGCTAAACCTTATGCATGAAACCACT
GATAAGAATTTATCACCTGATGGGCAATATGTGCCTAGAATCATGTTTGTAGACCCTTCTTT
AACAGTTAGAGCTGACATAGCTGGAAGATACTCTAACAGATTGTACACATATGAGCCTCGGG
ATTTACCCCTATTGATAGAAAACATGAAGAAAGCATTAAGACTTATTCAGTCAGAGCTA**TAA**
GAGATGATGGAAAAAAGCCTTCACTTCAAAGAAGTCAAATTTTCATGAAGAAAACCTTCTGGCA
CATTGACAAATACTAAATGTGCAAGTATATAGATTTTGTAAATATTACTATTTAGTTTTTTTA
ATGTGTTTGCAATAGTCTTATTAAATAAATGTTTTTTTAAATCTGA

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FIGURE 28

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64896

<subunit 1 of 1, 166 aa, 1 stop

<MW: 19171, pI: 8.26, NX(S/T): 1

MMLHSALGLCLLLVTVSSNLAIKKEKRPPQTLSRGWGDDITWVQTYEEGLFYAQKSKKPL
MVIHHLEDCQYSQALKKVFAQNEEQEMAQNKFIMLNLMHETTDKNLSPDGQYVPRIMFVDP
SLTVRADIAGRYSNRLYTYEPRDLPLLIENMKKALRLIQSEL

Important features:

Signal peptide:

amino acids 1-23

N-myristoylation site.

amino acids 51-57

FIGURE 29

TAAAACAGCTACAATATTCCAGGGCCAGTCACTTGCCATTTCTCATAACAGCGTCAGAGAGA
AAGAACTGACTGAAACGTTTGAGATGAAGAAAGTTCTCCTCCTGATCACAGCCATCTTGGCA
GTGGCTGTTGGTTTCCCAGTCTCTCAAGACCAGGAACGAGAAAAAAGAAGTATCAGTGACAG
CGATGAATTAGCTTCAGGGTTTTTTGTGTTCCCTTACCCATATCCATTTCGCCCACCTCCAC
CAATTCCATTTCCAAGATTTCCATGGTTTAGACGTAATTTTCCTATTCCAATACCTGAATCT
GCCCCTACAACCTCCCCTTCCTAGCGAAAAGTAAACAAGAAGGATAAGTCACGATAAACCTGG
TCACCTGAAATTGAAATTGAGCCACTTCCTTGAAGAATCAAAATTCCTGTTAATAAAAGAAA
AACAAATGTAATTGAAATAGCACACAGCATTCTCTAGTCAATATCTTTAGTGATCTTCTTTA
ATAAACATGAAAGCAAAGATTTTGGTTTCTTAATTTCCACA

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FIGURE 30

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71290

><subunit 1 of 1, 85 aa, 1 stop

><MW: 9700, pI: 9.55, NX(S/T): 0

MKKVLLLLITAILAVAVGFPVSQDQEREKRSISDSDELASGFFVFPYPYPFRPLPPIPFPRFP
WFRRNFPIPIPIESAPTTPLPSEK

Important features of the protein:

Signal peptide:

amino acids 1-17

Homologous region to B3-hordein:

amino acids 47-85

FIGURE 31

CGGACGCGTGGGCGGGCGCGCCGGGAGGGACCGGCGGGCGGC**AT**GGGCGGGGGGCCCTGGGAT
GCGGGCCCCGTCTCGCCGCCTGCTGCCGCTGTTGCTGCTGCTCGGCCTGGCCCCGCGGCGCCGC
GGGAGCGCCGGGCCCCGACGGTTTAGACGTCTGTGCCACTTGCCATGAACATGCCACATGCC
AGCAAAGAGAAGGGAAGAAGATCTGTATTTGCAACTATGGATTTGTAGGGAACGGGAGGACT
CAGTGTGTTGATAAAAAATGAGTGCCAGTTTGGAGCCACTCTTGTCTGTGGGAACACACATC
TTGCCACAACACCCCCGGGGGCTTCTATTGCATTTGCCTGGAAGGATATCGAGCCACAAACA
ACAACAAGACATTCATTCCCAACGATGGCACCTTTTGTACAGACATAGATGAGTGTGAAGTT
TCTGGCCTGTGCAGGCATGGAGGGCGATGCGTGAACACTCATGGGAGCTTTGAATGCTACTG
TATGGATGGATACTTGCCAAGGAATGGACCTGAACCTTTCCACCCGACCACCGATGCCACAT
CATGCACAGAAATAGACTGTGGTACCCCTCCTGAGGTTCCAGATGGCTATATCATAGGAAAT
TATACGTCTAGTCTGGGCAGCCAGGTTCTGTTATGCTTGCAGAGAAGGATTCTTCAGTGTTC
AGAAGATACAGTTTCAAGCTGCACAGGCCTGGGCACATGGGAGTCCCCAAAATTACATTGCC
AAGAGATCAACTGTGGCAACCCTCCAGAAATGCGGCACGCCATCTTGGTAGGAAATCACAGC
TCCAGGCTGGGCGGTGTGGCTCGCTATGTCTGTCAAGAGGGCTTTGAGAGCCCTGGAGGAAA
GATCACTTCTGTTTGCACAGAGAAAGGCACCTGGAGAGAAAGTACTTTAACATGCACAGAAA
TTCTGACAAAGATTAATGATGTATCACTGTTTAAATGATACCTGTGTGAGATGGCAAATAAAC
TCAAGAAGAATAAACCCCAAGATCTCATATGTGATATCCATAAAAGGACAACGGTTGGACCC
TATGGAATCAGTTCGTGAGGAGACAGTCAACTTGACCACAGACAGCAGGACCCCAAGAGTGT
GCCTAGCCCTGTACCCAGGCACCAACTACACCGTGAACATCTCCACAGCACCTCCCAGGCGC
TCGATGCCAGCCGTCATCGGTTTCCAGACAGCTGAAGTTGATCTCTTAGAAGATGATGGAAG
TTTCAATATTTCAATATTTAATGAAACTTGTTTGAATTGAACAGGCGTTCTAGGAAAGTTG
GATCAGAACACATGTACCAATTTACCGTTCTGGGTGAGAGGTGGTATCTGGCTAACTTTTCT
CATGCAACATCGTTTAACTTTCACAACGAGGGAACAAGTGCCTGTAGTGTGTTTGGATCTGTA
CCCTACGACTGATTATACGGTGAATGTGACCCTGCTGAGATCTCCTAAGCGGCACCTCAGTGC
AAATAACAATAGCAACTCCCCAGCAGTAAACAGACCATCAGTAACATTTTCAGGATTTAAT
GAAACCTGCTTGAGATGGAGAAGCATCAAGACAGCTGATATGGAGGAGATGTATTTATTCCA
CATTTGGGGCCAGAGATGGTATCAGAAGGAATTTGCCAGGAAATGACCTTTAATATCAGTA
GCAGCAGCCGAGATCCCGAGGTGTGCTTGGACCTACGTCCGGGTACCAACTACAATGTCAGT
CTCCGGGCTCTGTCTTCGGAACCTTCCTGTGGTGCATCTCCCTGACAACCCAGATAACAGAGCC
TCCCCTCCCGGAAGTAGAATTTTTTTACGGTGCACAGAGGACCTCTACCACGCCTCAGACTGA
GGAAAGCCAAGGAGAAAAATGGACCAATCAGTTCATATCAGGTGTTAGTGCTTCCCCTGGCC
CTCCAAAGCACATTTTCTTGTGATTCTGAAGGCGCTTCCTCCTTCTTTAGCAACGCCTCTGA
TGCTGATGGATACGTGGCTGCAGAACTACTGGCCAAAGATGTTCCAGATGATGCCATGGAGA
TACCTATAGGAGACAGGCTGTACTATGGGGAATATTATAATGCACCCTTGAAAAGAGGGAGT
GATTACTGCATTATATTACGAATCACAAGTGAATGGAATAAGGTGAGAAGACACTCCTGTGC
AGTTTGGGCTCAGGTGAAAGATTCTGTCATCATGCTGCTGCAGATGGCGGGTGTGGACTGG
GTTCCCTGGCTGTTGTGATCATTCTCACATTCCTCTCCTTCTCAGCGGTG**TGA**TGGCAGATG
GACACTGAGTGGGGAGGATGCACTGCTGCTGGGCAGGTGTTCTGGCAGCTTCTCAGGTGCCC
GCACAGAGGCTCCGTGTGACTTCCGTCCAGGGAGCATGTGGGCCTGCAACTTTCTCCATTCC
CAGCTGGGCCCCATTCCCTGGATTTAAGATGGTGGCTATCCCTGAGGAGTCACCATAAGGAGA
AACTCAGGAATTCTGAGTCTTCCTGCTACAGGACCAGTTCTGTGCAATGAACTTGAGACT
CCTGATGTACACTGTGATATTGACCGAAGGCTACATACAGATCTGTGAATCTTGGCTGGGAC
TTCTCTGAGTGATGCCTGAGGGTCAGCTCCTCTAGACATTGACTGCAAGAGAATCTCTGCA
ACCTCCTATATAAAAGCATTCTGTTAATTTCATTTCAGAATCCATTCTTTACAATATGCAGTG
AGATGGGCTTAAGTTTGGGCTAGAGTTTGACTTTATGAAGGAGGTCATTGAAAAAGAGACA
GTGACGTAGGCAAATGTTTCAAGCACTTTAGAAACAGTACTTTTCTTATAATTAGTTGATAT
ACTAATGAGAAAATATACTAGCCTGGCCATGCCAATAAGTTTCTGCTGTGTCTGTTAGGCA
GCATTGCTTTGATGCAATTTCTATTGTCCTATATATTCAAAGTAATGTCTACATTCCAGTA
AAAATATCCCGTAATTAAAAA

FIGURE 32

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96031
><subunit 1 of 1, 747 aa, 1 stop
><MW: 82710, pI: 6.36, NX(S/T): 18
MGRGPWDAGPSRRLPLLLLLGLARGAAGAPGPDGLDVCATCHEHATCQQREGKKICICNYG
FVGNGRTQCVDKNECQFGATLVCGNHTSCHNTPGGFYCICLEGYRATNNNKTFIPNDGTFCF
DIDECEVSGLCRHHGRCVNTHGSEFCYCMDGYLPRNGPEPFHPTTDDATSCTEIDCGTPPEVP
DGYIIGNYTSSLGSQVRYACREGFFSVPEDTVSSCTGLGTWESPCLHCQEINCGNPPEMRHA
ILVGNHSSRLGGVARYVCQEGFESPGGKITSVCTEKG TWRESTLTCTEILT KINDVSLFNDT
CVRWQINSRRINPKISYVISIKQRLDPMESVREETVNLTTDSRTPEVCLALYPGTNYTVNI
STAPRRSMPAVIGFQTAEVDLLEDDGSFNISIFNETCLKLNRRSRKVGSEHMYQFTVLGQR
WYLANFSHATSFNFTTREQVPVVCCLDLYPTTDYTVNVTLLRSPKRHSVQITIATPPAVKQTI
SNISGFNETCLRWSIKTADMEEMYLEFHIWGQRWYQKEFAQEMTFNIISSSSRDPEVCLDLRP
GTNYNVSLRALSSELPVVISLTTQITEPPLPEVEFFTVHRGPLPRLRLRKAKEKNGPISSYQ
VLVLPLALQSTFSCDSEGASSFFSNASDADGYVAAELLAKDVPDDAMEIPIGDRLYYGEYYN
APLKRGS DYCIILRITSEWNKVR RHSCAVWAQVKDSSLMLLQMAGVGLGSLAVVIILTFLSF
SAV
```

Important features of the protein:

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 718-740

N-glycosylation sites.

amino acids 87-91, 112-116, 193-197, 253-257, 308-312, 348-352, 367-371, 371-375, 402-406, 407-411, 439-443, 447-451, 470-474, 498-502, 503-507, 542-546, 563-567, 645-649

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 478-482, 686-690, 705-709

Tyrosine kinase phosphorylation site.

amino acids 419-427

N-myristoylation sites.

amino acids 22-28, 35-41, 65-71, 86-92, 96-102, 120-126, 146-152, 192-198, 252-258, 274-280, 365-371, 559-565, 688-694, 727-733.

Amidation site.

amino acids 52-56

Aspartic acid and asparagine hydroxylation sites.

amino acids 91-103, 141-153.

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 624-635

Cytochrome c family heme-binding site signature.

amino acids 39-45

Calcium-binding EGF-like domain proteins pattern proteins.

amino acids 85-106, 135-156

Receptor tyrosine kinase class V proteins:

amino acids 389-422

FIGURE 33

GGAAAAGGTACCCGCGAGAGACAGCCAGCAGTTCTGTGGAGCAGCGGTGGCCGGCTAGG**ATG**
GGCTGTCTCTGGGGTCTGGCTCTGCCCCTTTTCTTCTTCTGCTGGGAGGTTGGGGTCTCTGG
GAGCTCTGCAGGCCCCAGCACCCGCGAGAGCAGACACTGCGATGACAACGGACGACACAGAAG
TGCCCGCTATGACTCTAGCACCGGGCCACGCCGCTCTGGAAACTCAAACGCTGAGCGCTGAG
ACCTCTTCTAGGGCCTCAACCCAGCCGGCCCCATTCCAGAAGCAGAGACCAGGGGAGCCAA
GAGAATTTCCCCTGCAAGAGAGACCAGGAGTTTCACAAAAACATCTCCCAACTTCATGGTGC
TGATCGCCACCTCCGTGGAGACATCAGCCGCCAGTGGCAGCCCCGAGGGAGCTGGAATGACC
ACAGTTCAGACCATCACAGGCAGTGATCCCGAGGAAGCCATCTTTGACACCCTTTGCACCGA
TGACAGCTCTGAAGAGGCAAAGACACTCACAATGGACATATTGACATTGGCTCACACCTCCA
CAGAAGCTAAGGGCCTGTCCTCAGAGAGCAGTGCCTCTTCCGACGGCCCCCATCCAGTCATC
ACCCCGTCAACGGGCCTCAGAGAGCAGCGCCTCTTCCGACGGCCCCCATCCAGTCATCACCCC
GTCACGGGCCTCAGAGAGCAGCGCCTCTTCCGACGGCCCCCATCCAGTCATCACCCCGTCAT
GGTCCCCGGGATCTGATGTCACTCTCCTCGCTGAAGCCCTGGTGACTGTCACAAACATCGAG
GTTATTAATTGCAGCATCACAGAAATAGAAACAACAACCTTCCAGCATCCCTGGGGCCTCAGA
CATAGATCTCATCCCCACGGAAGGGGTGAAGGCCTCGTCCACCTCCGATCCACCAGCTCTGC
CTGACTCCACTGAAGCAAAACCACACATCACTGAGGTACAGCCTCTGCCGAGACCCTGTCC
ACAGCCGGCACCACAGAGTCAGCTGCACCTCATGCCACGGTTGGGACCCCACTCCCCACTAA
CAGCGCCACAGAAAGAGAAGTGACAGCACCCGGGGCCACGACCCTCAGTGGAGCTCTGGTCA
CAGTTAGCAGGAATCCCCTGGAAGAAACCTCAGCCCTCTCTGTTGAGACACCAAGTTACGTC
AAAGTCTCAGGAGCAGCTCCGGTCTCCATAGAGGCTGGGTCAGCAGTGGGCAAAACAACCTTC
CTTTGCTGGGAGCTCTGCTTCCTCCTACAGCCCCTCGGAAGCCGCCCTCAAGAACTTCACCC
CTTCAGAGACACCGACCATGGACATCGCAACCAAGGGGGCCCTTCCCCACCAGCAGGGACCCT
CTTCCTTCTGTCCCTCCGACTACAACCAACAGCAGCCGAGGGACGAACAGCACCTTAGCCAA
GATCACAACCTCAGCGAAGACCACGATGAAGCCCCAACAGCCACGCCCACGACTGCCCGGAC
GAGGCCGACCACAGACG**TGA**GTGCAGGTGAAAATGGAGGTTTCCTCCTCCTGCGGCTGAGTG
TGGCTTCCCCGGAAGACCTCACTGACCCCAGAGTGGCAGAAAGGCTGATGCAGCAGCTCCAC
CGGGAACCTCACGCCCCACGCGCCTCACTTCCAGGTCTCCTTACTGCGTGTCAGGAGAGGCTA
ACGGACATCAGCTGCAGCCAGGCATGTCCCGTATGCCAAAAGAGGGTGCTGCCCCCTAGCCTG
GGCCCCCACCAGACAGACTGCAGCTGCGTTACTGTGCTGAGAGGTACCCAGAAGGTTCCCATG
AAGGGCAGCATGTCCAAGCCCCTAACCCAGATGTGGCAACAGGACCCTCGCTCACATCCAC
CGGAGTGTATGTATGGGGAGGGGCTTCACCTGTTCCAGAGGTGTCCTTGGACTCACCTTGG
CACATGTTCTGTGTTTCAGTAAAGAGAGACCTGATCACCCATCTGTGTGCTTCCATCCTGCA
TTAAAATTCACCTCAGTGTGGCCCCAAAAAAA

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FIGURE 34

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108722

><subunit 1 of 1, 482 aa, 1 stop

><MW: 49060, pI: 4.74, NX(S/T): 4

MGCLWGLALPLFFFCWEVGVSGSSAGPSTRRADTAMTTDDTEVPAMTLAPGHAALETQTL
ETSSRASTPAGPIPEAETRGAKRISPARETRSF TKTS PNFVLIATSVETSAASGSPEGAGM
TTVQTITGSDPEEAI FDTLCTDD SSEEAKLTMDILT LAHTSTEAKGLSSESSASSDGPHPV
ITPSRASESSASSDGPHPVITPSRASESSASSDGPHPVITPSWSPGSDVTLLAEALVTVTNI
EVINCSITEIETTTSSIPGASDIDLIPTEGVKASSTSDPPALPDSTEAKPHITEVTASAETL
STAGTTESAAPHATVGTPLPTNSATEREVTAPGATTL SGALVTVSRNPLEETSALSVETPSY
VKVSGAAPVSIEAGSAVGKTTSFAGSSASSYSPSEAALKNETPSETPTMDIATKGPFPTSRD
PLPSVPPTTTNSSRGTNSTLAKITTS AKTTMKPQQPRPRLPGRGRPQT

Important features of the protein:

Signal peptide:

amino acids 1-25

N-glycosylation sites.

amino acids 252-256, 445-449, 451-455

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 84-88

N-myristoylation sites.

amino acids 2-8, 19-25, 117-123, 121-127, 232-238, 278-284,
314-320, 349-355, 386-392, 397-403, 449-455

ATP/GTP-binding site motif A (P-loop).

amino acids 385-393

FIGURE 35

GCCTCTGAATTGTTGGGCAGTCTGGCAGTGGAGCTCTCCCCGGTCTGACAGCCACTCCAGAG
GCCATGCTTCGTTTCTTGCCAGATTTGGCTTTCAGCTTCCTGTTAATTCTGGCTTTGGGCCA
GGCAGTCCAATTTCAAGAATATGTCTTTCTCCAATTTCTGGGCTTAGATAAGGCGCCTTCAC
CCCAGAAGTTCCAACCTGTGCCTTATATCTTGAAGAAAATTTTCCAGGATCGCGAGGCAGCA
GCGACCACTGGGGTCTCCCGAGACTTATGCTACGTAAAGGAGCTGGGCGTCCGCGGGAATGT
ACTTCGCTTTCTCCCAGACCAAGGTTTCTTTCTTTACCCAAAGAAAATTTCCCAAGCTTCCT
CCTGCCTGCAGAAGCTCCTCTACTTTAACCTGTCTGCCATCAAAGAAAGGGAACAGTTGACA
TTGGCCCAGCTGGGCCTGGACTTGGGGCCCAATTCTTACTATAACCTGGGACCAGAGCTGGA
ACTGGCTCTGTTCCCTGGTTCAGGAGCCTCATGTGTGGGGCCAGACCACCCCTAAGCCAGGTA
AAATGTTTGTGTTGCGGTCAGTCCCATGGCCACAAGGTGCTGTTCACTTCAACC'TGC'T'GGA'T
GTAGCTAAGGATTGGAATGACAACCCCCGGAAAAATTTTCGGGTATTCCTGGAGATACTGGT
CAAAGAAGATAGAGACTCAGGGGTGAATTTTCAGCCTGAAGACACCTGTGCCAGACTAAGAT
GCTCCCTTCATGCTTCCCTGCTGGTGGTGA CTCTCAACCCTGATCAGTGCCACCCTTCTCGG
AAAAGGAGAGCAGCCATCCCTGTCCCCAAGCTTTCTTGTAAGAACCTCTGCCACCGTCACCA
GCTATTCAATTAACCTCCGGGACCTGGGTGTCACAAAGTGGATCATTGCCCCCAAGGGGTTCA
TGGCAAATTACTGCCATGGAGAGTGTCCCTTCTCACTGACCATCTCTCTCAACAGCTCCAAT
TATGCTTTCATGCAAGCCCTGATGCATGCCGTTGACCCAGAGATCCCCCAGGCTGTGTGTAT
CCCCACCAAGCTGTCTCCCATTTCCATGCTCTACCAGGACAATAATGACAATGTCATTCTAC
GACATTATGAAGACATGGTAGTCGATGAATGTGGGTGTGGGTAGGATGTCAGAAATGGGAAT
AGAAGGAGTGTTCTTAGGGTAAATCTTTTAATAAACTACCTATCTGGTTTATGACCACTTA
GATCGAAATGTC

FIGURE 36

MLRFLPDLAFSFLLILALGQAVQFQEYVFLQFLGLDKAPSPQKFQPVPIYILKKIFQDREAAA
TTGVSRDLCYVKELGVRGNVLRFLPDQGFFLYPKKISQASSCLQKLLYFNLSAIKEREQLTL
AQLGLDLGPNSYYNLGPELELALFLVQEPHVWGQTTPKPGKMFVLRVWPWPQGAVHFNLLDV
AKDWNDNPRKNFGLFLEILVKEDRDSGVNFQPEDTCARLRCSLHASLLVVTNLNPDQCHPSRK
RRAAIPVPKLSCKNLCHRHQLFINFRDLGWHKWIIAPKGFMANYPHGECPFSLTISLNSSNY
AFMQALMHAVDPEIPQAVCIPTKLSPISMPLYQDNNDNVILRHYEDMVVDECGCG

Important features of the protein:**Signal peptide:**

amino acids 1-21

N-glycosylation sites.

amino acids 112-116, 306-310

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 96-100

N-myristoylation site.

amino acids 77-83

TGF-beta family proteins.

amino acids 264-299, 327-341, 345-364

FIGURE 37

CACTTTCTCCCTCTCTTCCTTTACTTTTCGAGAAACCGCGCTTCCGCTTCTGGTCGCAGAGAC
 CTCGGAGACCGCGCCGGGGAGACGGAGGTGCTGTGGGTGGGGGGGACCTGTGGCTGCTCGTA
 CCGCCCCCACCCTCCTCTTCTGCACTGCCGTCTCCGGAAGACCTTTTCCCCTGCTCTGTT
 TCCTTCACCGAGTCTGTGCATCGCCCCGGACCTGGCCGGGAGGAGGCTTGGCCGGCGGGAGA
 TGCTCTAGGGGCGGCGCGGGAGGAGCGGCCGGCGGGACGGAGGGCCCGGCAGGAAG**ATGGGC**
 TCCCGTGGACAGGGACTCTTGCTGGCGTACTGCCTGCTCCTTGCCTTTGCCTCTGGCCTGGT
 CCTGAGTCGTGTGCCCCATGTCCAGGGGGGAACAGCAGGAGTGGGAGGGGACTGAGGAGCTGC
 CGTCGCCTCCGGACCATGCCGAGAGGGCTGAAGAACAACATGAAAAATACAGGCCCAGTCAG
 GACCAGGGGCTCCCTGCTTCCCGGTGCTTGCCTGCTGTGACCCCGGTACCTCCATGTACCC
 GCGACCGCCGTGCCCCAGATCAACATCACTATCTTGAAAGGGGAGAAGGGTGACCGCGGAG
 ATCGAGGCCTCCAAGGGGAAATATGGCAAACAGGCTCAGCAGGGGGCCAGGGGGCCACACTGGA
 CCCAAAGGGCAGAAGGGCTCCATGGGGGCCCTGGGGAGCGGTGCAAGAGCCACTACGCCGC
 CTTTTCGGTGGGCCCGGAAGAAGCCCATGCACAGCAACCACTACTACCAGACGGTGATCTTCG
 ACACGGAGTTTCGTGAACCTCTACGACCACTTCAACATGTTTACCGGCAAGTTCTACTGCTAC
 GTGCCCGGCCTCTACTTCTTCAGCCTCAACGTGCACACCTGGAACCAGAAGGAGACCTACCT
 GCACATCATGAAGAACGAGGAGGAGGTGGTGATCTTGTTCGCGCAGGTGGGCGACCGCAGCA
 TCATGCAAAGCCAGAGCCTGATGCTGGAGCTGCGAGAGCAGGACCAGGTGTGGGTACGCCTC
 TACAAGGGCGAACGTGAGAACGCCATCTTCAGCGAGGAGCTGGACACCTACATCACCTTCAG
 TGGCTACCTGGTCAAGCACGCCACCGAGCCCT**TAG**CTGGCCGGCCACCTCCTTTCTCTCGCC
 ACCTTCCACCCCTGCGCTGTGCTGACCCACCGCCTCTTCCCCGATCCCTGGACTCCGACTC
 CCTGGCTTTGGCATTTCAGTGAGACGCCCTGCACACACAGAAAGCCAAAGCGATCGGTGCTCC
 CAGATCCCGCAGCCTCTGGAGAGAGCTGACGGCAGATGAAATCACCAGGGCGGGGCACCCGC
 GAGAACCCTCTGGGACCTTCCGCGGCCCTCTCTGCACACATCCTCAAGTGACCCCGCACGGC
 GAGACGCGGGGTGGCGGCAGGGCGTCCCAGGGTGCGGCACCGCGGCTCCAGTCCTTGGAATA
 ATTAGGCAAATTCTAAAGGTCTCAAAGGAGCAAAGTAAACCGTGGAGGACAAAGAAAAGGG
 TTGTTATTTTTGTCTTTCCAGCCAGCCTGCTGGCTCCCAAGAGAGAGGCCTTTTCAGTTGAG
 ACTCTGCTTAAGAGAAGATCCAAAGTTAAAGCTCTGGGGTCAGGGGAGGGGGCCGGGGGCAGG
 AACTACCTCTGGCTTAATTCTTTTAAAGCCACGTAGGAACCTTTCTTGAGGGATAGGTGGACC
 CTGACATCCCTGTGGCCTTGCCCAAGGGCTCTGCTGGTCTTTCTGAGTCACAGCTGCGAGGT
 GATGGGGGCTGGGGCCCCAGGCGTCAGCCTCCCAGAGGGACAGCTGAGCCCCCTGCCTTGGC
 TCCAGGTTGGTAGAAGCAGCCGAAGGGCTCCTGACAGTGGCCAGGGACCCCTGGGTCCCCCA
 GGCCTGCAGATGTTTCTATGAGGGGCAGAGCTCCTTGGTACATCCATGTGTGGCTCTGCTCC
 ACCCCTGTGCCACCCAGAGCCCTGGGGGGTGGTCTCCATGCCCTGCCACCCTGGCATCGGCT
 TTCTGTGCCGCTCCACACAAATCAGCCCCAGAAGGCCCGGGGCCTTGGCTTCTGTTTTT
 TATAAACACCTCAAGCAGCACTGCAGTCTCCATCTCCTCGTGGGCTAAGCATCACCGCTT
 CCACGTGTGTTGTGTTGGTTGGCAGCAAGGCTGATCCAGACCCCTTCTGCCCCACTGCCCT
 CATCCAGGCCTCTGACCAGTAGCCTGAGAGGGGCTTTTTCTAGGCTTCAGAGCAGGGGAGAG
 CTGGAAGGGGCTAGAAAGCTCCCGCTTGTCTGTTTCTCAGGCTCCTGTGAGCCTCAGTCCTG
 AGACCAGAGTCAAGAGGAAGTACACGTCCCAATCACCCGTGTCAGGATTCACTCTCAGGAGC
 TGGGTGGCAGGAGAGGCAATAGCCCCCTGTGGCAATTGCAGGACCAGCTGGAGCAGGGTTGCG
 GTGTCTCCACGGTGCTCTCGCCCTGCCCATGGCCACCCAGACTCTGATCTCCAGGAACCC
 ATAGCCCCTCTCCACCTCACCCCATGTTGATGCCAGGGTCACTCTTGCTACCCGCTGGGCC
 CCCAAACCCCGCTGCCTCTCTTCCCTTCCCCCATCCCCACCTGGTTTTGACTAATCCTGC
 TTCCCTCTCTGGGCCTGGCTGCCGGGATCTGGGGTCCCTAAGTCCCTCTCTTTAAAGAACTT
 CTGCGGGTCAGACTCTGAAGCCGAGTTGCTGTGGGCGTGCCCGGAAGCAGAGCGCCACACTC
 GCTGCTTAAGCTCCCCAGCTCTTTCCAGAAAACATTAAACTCAGAATTGTGTTTTCAA

38/75

FIGURE 38

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41234
><subunit 1 of 1, 281 aa, 1 stop
><MW: 31743, pI: 6.83, NX(S/T): 1
MGSRGQGLLLAYCLLLAFASGLVLSRVPHVQGEQQEWEGTEELPSPPDHAERAEEQHEKYRP
SQDQGLPASRCLRCCDPGTSMYPATAVPQINITILKGEKGDRGDRGLQGKYGKTGSAGARGH
TGPKGQKGSMGAPGERCKSHYAAFSVGRKKPMHSNHYYQTVIFDTEFVNLYDHFNMFTGKFY
CYVPGLYFFSLNVHTWNQKETYLHIMKNEEEVVILFAQVGDRSIMQSQSLMLELREQDQVWV
RLYKGERENAI FSEELDTYITFSGYLVKHATEP
```

Signal sequence.

amino acids 1-25

N-glycosylation site.

amino acids 93-97

N-myristoylation sites.

amino acids 7-13, 21-27, 67-73, 117-123, 129-135

Amidation site.

amino acids 150-154

Cell attachment sequence.

amino acids 104-107

FIGURE 39

GAATTCGGCACGAGGGAAGAAGAGAAAGAAAATCTCCGGGGCTGCTGGGAGCATATAAAGAA
GCCCTGTGGCCTTGCTGGTTTTACCATCCAGACCAGAGTCAGGCCACAGACGGACATGGCTG
CTCAAGGCTGGTCCATGCTCCTGCTGGCTGTCCTTAACCTAGGCATCTTCGTCCGTCCCTGT
GACACTCAAGAGCTACGATGTCTGTGTATTCAGGAACACTCTGAATTCATTCCTCTCAAAC
CATTA AAAATATAATGGTGATATTCGAGACCATTTACTGCAACAGAAAGGAAGTGATAGCAG
TCCCAAAAATGGGAGTATGATTTGTTTGGATCCTGATGCTCCATGGGTGAAGGCTACTGTT
GGCCAATTACTAACAGGTTCTACCTGAGGACCTCAAACAAAAGGAATTTCCACCGGCAAT
GAAGCTTCTGTATAGTGTTGAGCATGAAAAGCCTCTATATCTTTCATTTGGGAGACCTGAGA
ACAAGAGAATATTTCCCTTTCCAATTCGGGAGACCTCTAGACACTTTGCTGATTTAGCTCAC
AACAGTGATAGGAATTTTCTACGGGACTCCAGTGAAGTCAGCTTGACAGGCAGTGATGCCTA
AAAGCCACTCATGAGGCCAAAGAGTTTCAAGGAAGCTCTCCTCCTGGAGTTTTGGCGTTCTCA
TTCTTATACTCTATTCCCGCGTTAGTCTGGTGTATGGATCTATGAGCTCTCTTTTAATATTT
TATTATAAATGTTTTATTTACTTAACTTCCTAGTGAATGTTTCACAGGTGACTGCTCCCCCAT
CCCCATTTCTTGATATTACATATAATGGCATCATATACCCCTTTATTGACTGACAACTACT
CAGATTGCTTAACATTTTGTGCTTCAAAGTCTTATCCCACTCCACTATGGGCTGTTACAGAG
TGCATCTCGGTGTAGAGCAAGGCTCCTTGTCTTCAGTGCCCCAGGGTGAAATACTTCTTTGA
AAAATTTTCATTCATCAGAAAATCTGAAATAAAAATATGTCTTAATTGAG

40/75

FIGURE 40

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73838
><subunit 1 of 1, 167 aa, 1 stop
><MW: 19091, pI: 7.48, NX(S/T): 1
MAAQGWSMLLLAVLNLGIFVRPCDTQELRCLCIQEHSEFIPLKLIK NIMVIFETIYCNRKEV
IAVPKNGSMICLDPDAPWVKATVGPITNRFLPEDLKQKEFPPAMKLLYSVEHEKPLYLSFGR
PENKRIFPFPPIRETSRHFADLAHNSDRNFLRDSSEVSLTGSDA
```

Important features of the protein:

Signal peptide:

amino acids 1-25

N-glycosylation site.

amino acids 68-72

N-myristoylation site.

amino acids 69-75

Small cytokines (intercrine/chemokine) C-x-C subfamily signature

amino acids 40-85

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FIGURE 41

CAGACATGGCTCAGTCACTGGCTCTGAGCCTCCTTATCCTGGTTCTGGCCTTTGGCATCCCC
AGGACCCAAGGCAGTGATGGAGGGGCTCAGGACTGTTGCCTCAAGTACAGCCAAAGGAAGAT
TCCCGCCAAGGTTGTCCGCAGCTACCGGAAGCAGGAACCAAGCTTAGGCTGCTCCATCCCAG
CTATCCTGTTCTTGCCCCGCAAGCGCTCTCAGGCAGAGCTATGTGCAGACCCAAAGGAGCTC
TGGGTGCAGCAGCTGATGCAGCATCTGGACAAGACACCATCCCCACAGAAACCAGCCCAGGG
CTGCAGGAAGGACAGGGGGGCCTCCAAGACTGGCAAGAAAGGAAAGGGCTCCAAAGGCTGCA
AGAGGACTGAGCGGTCACAGACCCCTAAAGGGCCATAGCCCAGTGAGCAGCCTGGAGCCCTG
GAGACCCCAACCAGCCTCACCAGCGCTTGAAGCCTGAACCCAAGATGCAAGAAGGAGGCTATG
CTCAGGGGGCCCTGGAGCAGCCACCCCATGCTGGCCTTGCCACACTCTTTCTCCTGCTTTAAC
CACCCCATCTGCATTCCCAGCTCTACCCTGCATGGCTGAGCTGCCCACAGCAGGCCAGGTCC
AGAGAGACCGAGGAGGGAGAGTCTCCCAGGGAGCATGAGAGGAGGCAGCAGGACTGTCCCCT
TGAAGGAGAATCATCAGGACCCTGGACCTGATACGGCTCCCCAGTACACCCACCTCTTCCT
TGTAATATGATTTATACCTAACTGAATAAAAAGCTGTTCTGTCTTCCCNCCCA

42/75

FIGURE 42

><MW: 14646, pI: 10.45, NX(S/T): 0

MAQSLALSLLILVLAFGIPRTQGSDGGAQDCCLKYSQRKIPAKVVRSYRKQEPSLGCSIPAI
LFLPRKRSQAELCADPKELWVQQQLMQHLDKTPSPQKPAQGCRKDRGASKTGKKKGKSGKCKR
TERSQTPKGP

Important features of the protein:

Signal peptide:

amino acids 1-17

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 67-71

N-myristoylation sites.

amino acids 17-23, 23-29, 27-33, 108-114, 118-124, 121-127

Amidation site.

amino acids 112-116

Small cytokines.

amino acids 51-91

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FIGURE 43

AAGGAGCAGCCCGCAAGCACCAAGTGAGAGGCATGAAGTTACAGTGTGTTTCCCTTTGGCTC
CTGGGTACAATACTGATATTGTGCTCAGTAGACAACCACGGTCTCAGGAGATGTCTGATTTT
CACAGACATGCACCATATAGAAGAGAGTTTCCAAGAAATCAAAAGAGCCATCCAAGCTAAGG
ACACCTTCCCAAATGTCACCTATCCTGTCCACATTGGAGACTCTGCAGATCATTAAGCCCTTA
GATGTGTGCTGCGTGACCAAGAACCTCCTGGCGTTCTACGTGGACAGGGTGTTCAGGATCA
TCAGGAGCCAAACCCCAAATCTTGAGAAAAATCAGCAGCATTGCCAACTCTTTCCTCTACA
TGCAGAAAACCTCTGCGGCAATGTCAGGAACAGAGGCAGTGTCACTGCAGGCAGGAAGCCACC
AATGCCACCAGAGTCATCCATGACAACTATGATCAGCTGGAGGTCCACGCTGCTGCCATTAA
ATCCCTGGGAGAGCTCGACGTCTTCTAGCCTGGATTAATAAGAATCATGAAGTAATGTTCT
CAGCTTGATGACAAGGAACCTGTATAGTGATCCAGGGATGAACACCCCCTGTGCGGTCTTACT
GTGGGAGACAGCCACCTTGAAGGGGAAGGAGATGGGGAAGGCCCTTGCAGCTGAAAGTCC
CACTGGCTGGCCTCAGGCTGTCTTATTCCGCTTGAAAATAGGC AAAAAGTCTACTGTGGTAT
TTGTAATAAACTCTATCTGCTGAAAGGGCCTGCAGGCCATCCTGGGAGTAAAGGGCTGCCTT
CCCATCTAATTTATTGTAAAGTCATATAGTCCATGTCTGTGATGTGAGCCAAGTGATATCCT
GTAGTACACATTGTACTGAGTGGTTTTTCTGAATAAATTCCATATTTTACCTATGA

FIGURE 44

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA92282
><subunit 1 of 1, 177 aa, 1 stop
><MW: 20452, pI: 8.00, NX(S/T): 2
MKLQCVSLWLLGTILILCSVDNHGLRRCLISTDMHHIEESFQEIKRAIQAKDTFPNVTILST
LETLQIIKPLDVCCVTKNLLAFYVDRVFKDHQEPNPKILRKISSIANSFLYMQKTLRQCQEQ
RQCHCRQEATNATRVIHDNYDQLEVHAAAIKSLGELDVFLAWINKNHEVMFSA

Signal sequence:

amino acids 1-18

N-glycosylation sites.

amino acids 56-60, 135-139

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 102-106

N-myristoylation site.

amino acids 24-30

Actinin-type actin-binding domain signature 1.

amino acids 159-169

45/75

FIGURE 46

MRSGCVVHVWILAGLWLAVAGRPLAFSDAGPHVHYGWDPIRLRHLYTSGPHGLSSCFLRI
RADGVVDCARGQSAHSLLEIKAVALLRTVAIKGVHVSRYLCMGADGKMQLLQYSEEDCAFEE
EIRPDGYNVYRSEKHRLPVSLSSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLESD
MFSSPLETDSMDPFGLVTGLEAVRSPSFEK

Signal peptide:

amino acids 1-22

Casein kinase II phosphorylation site.

amino acids 78-82, 116-120, 190-194, 204-208

N-myristoylation site.

amino acids 15-21, 54-60, 66-72, 201-207

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 48-59

FIGURE 47

GTCTGTTCCCAGGAGTCCTTCGGCGGCTGTTGTGTGTCAGTGGCCTGATCGCG**ATG**GGGACAAA
GGCGCAAGTCGAGAGGAACTGTTGTGCCTCTTCATATTGGCGATCCTGTTGTGCTCCCTGG
CATTGGGCAGTGTTACAGTGCACTCTTCTGAACCTGAAGTCAGAATTCCTGAGAATAATCCT
GTGAAGTTGTCCTGTGCCTACTCGGGCTTTTCTTCTCCCCGTGTGGAGTGGAAGTTTGACCA
AGGAGACACCACCAGACTCGTTTGCTATAATAACAAGATCACAGCTTCCTATGAGGACCGGG
TGACCTTCTTGCCAACTGGTATCACCTTCAAGTCCGTGACACGGGAAGACACTGGGACATAC
ACTTGTATGGTCTCTGAGGAAGGCGGCAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGT
GCTTGTGCCTCCATCCAAGCCTACAGTTAACATCCCCCTCCTCTGCCACCATTGGGAACCGGG
CAGTGCTGACATGCTCAGAACAAGATGGTTCCCCACCTTCTGAATACACCTGGTTCAAAGAT
GGGATAGTGATGCCCTACGAATCCCAAAAGCACCCGTGCCCTTCAGCAACTCTTTCCTATGTCCCT
GAATCCCACAACAGGAGAGCTGGTCTTTGATCCCCCTGTCAGCCTCTGATACTGGAGAATACA
GCTGTGAGGCACGGAATGGGTATGGGACACCCATGACTTCAAATGCTGTGCGCATGGAAGCT
GTGGAGCGGAATGTGGGGGTGTCATCGTGGCAGCCGTCCTTGTAACCCTGATTCTCCTGGGAAT
CTTGGTTTTTTGGCATCTGGTTTGCCTATAGCCGAGGCCACTTTGACAGAACAAAGAAAGGGA
CTTCGAGTAAGAAGGTGATTTACAGCCAGCCTAGTGCCCGAAGTGAAGGAGAATTCAAACAG
ACCTCGTCATTCCTGGTG**TGA**GCCTGGTCGGCTCACCGCCTATCATCTGCATTTGCCTTACT
CAGGTGCTACCGGACTCTGGCCCCCTGATGTCTGTAGTTTACAGGATGCCTTATTTGTCTTC
TACACCCACAGGGCCCCCTACTTCTTCGGATGTGTTTTTAATAATGTCAGCTATGTGCCCC
ATCCTCCTTCATGCCCTCCCTCCCTTTCCTACCACTGCTGAGTGGCCTGGAACCTGTTTAAA
GTGTTTATTCCCCATTTCTTTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCC
TTCTAAGTAGACAGCAAAAATGGCGGGGGTGCAGGAATCTGCACTCAACTGCCACCTGGC
TGGCAGGGATCTTTGAATAGGTATCTTGAGCTTGGTTCTGGGCTCTTTCCTTGTGTACTGAC
GACCAGGGCCAGCTGTTCTAGAGCGGGAATTAGAGGCTAGAGCGGCTGAAATGGTTGTTTGG
TGATGACACTGGGGTCCTTCCATCTCTGGGGCCCACTCTCTTCTGTCTTCCCATGGGAAGTG
CCACTGGGATCCCTCTGCCCTGTCCTCCTGAATACAAGCTGACTGACATTGACTGTGTCTGT
GGAAAATGGGAGCTCTTGTTGTGGAGAGCATAGTAAATTTTCAGAGAACTTGAAGCCAAAAG
GATTTAAAACCGCTGCTCTAAAGAAAAGAAAAGTGGAGGCTGGGCGCAGTGGCTCACGCCTG
TAATCCCAGAGGCTGAGGCAGGCGGATCACCTGAGGTCTGGGAGTTCGGGATCAGCCTGACCA
ACATGGAGAAACCCCTACTGGAAATACAAAGTTAGCCAGGCATGGTGGTGCATGCCTGTAGTC
CCAGCTGCTCAGGAGCCTGGCAACAAGAGCAAAACTCCAGCTCAAAAAAAAAAAAAAAAAA

48/75

FIGURE 48

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSLAYSGFSSPRVEW
KFDQGD TTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEEGGNSYGEVKV
KLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPSEYTWFKDGIVMPTNPKSTRAFSNS
SYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTTPM TSNAVRMEAVERNVGVIVA AVLVTLI
LLGILVFGIWFAYS RGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 238-255

N-glycosylation site.

amino acids 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 270-274

Casein kinase II phosphorylation site.

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,
193-197, 203-207, 287-291

N-myristoylation site.

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

49/75

50/75

FIGURE 50

MGAARLLPNLTLCLQLLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRI
SATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMKNRGKLGKPSGKSKDCVFTEIVLE
NNYTAFQNARHEGWFMFAFTRQGRPRQASRSRQNQREAHFIKRLYQGQLPFPNHAEKQKQFEF
VGSAPTRRTKRTRRPQPLT

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 9-13, 126-130

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 60-64

Casein kinase II phosphorylation site.

amino acids 65-69

Tyrosine kinase phosphorylation site.

amino acids 39-48, 89-97

N-myristoylation site.

amino acids 69-75, 188-194

Amidation site.

amino acids 58-62

HBGF/FGF family signature.

amino acids 103-128

FIGURE 51

GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACACAA
TCTATCAGGAAAGAAAGAAAGAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAGAAGA
AAAAAATC**ATG**AAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCAC
GGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCC
CCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATT
GACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGA
CAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCG
AGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAAC
CACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAATTTGTAGAGATTTT
TTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGAC
CAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGAC
GAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTC
CAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACCTATCCACCATACA
TTTCAGAAGCCAAGGGTACAGGTGTCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCC
TCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAA
GAAAGGGGTGAAAGTGGAAAACAGACCTTTCTCTCAAACTCATCTTCTTCAATGTCTCTG
AACATGACTATGGGAACTACACTTGCCTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGC
ATCATGCTATTTGGTCCAGGCGCCGTGAGCGAGGTGAGCAACGGCACGTGAGGAGGGCAGG
CTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGACCTGCTTCTCAAATTT**TGA**TGTGAGTGCC
ACTTCCCCACCCGGGAAAGGCTGCCGCCACCACCACCACCAACACAACAGCAATGGCAACAC
CGACAGCAACCAATCAGATATATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGA
AATTTGAGGGAGGGGAACAAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAA
AATTGCCTTGCAGATATTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGC
ACACCCGGCTTGGACCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAA
GGGCTCAGCCTCTCTGCCCACAGAGTGCCCCCACGTGGAACATTCTGGAGCTGGCCATCCCA
AATTCAATCAGTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGG
GCACTTTGGTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAA
AAAAA

FIGURE 52

MKTIQPKMHNSISWAI FTGLAALCLFQGVPVRS GDA TFPKAMDNVTVRQGESATLRCTIDNR
VTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNV DVYDEGPYTCSVQTDNHPK
TSRVHLIVQVSPKIVEISSDISINEGNNISLT CIATGRPEPTVTWRHISPKAVGFVSEDEYL
EIQGITREQSGDYEC SASNDVAAPV VRRVKVTVNYPPISEAKGTGVPVGQKGT LQCEASAV
PSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGN YTCVASNKLGH TNASIML
FGPGAVSEVSNGTSRRAGCVWLLPLLVLHLL LKF

Signal peptide:

amino acids 1-28

53/75

amino acids 301-304

FIGURE 55

AGCCAGGCAGCACATCACAGCGGGAGGAGCTGTCCCAGGTGGCCCAGCTCAGCA**ATGG**CAAT
GGGGGTCCCCAGAGTCATTCTGCTCTGCCTCTTTGGGGCTGCGCTCTGCCTGACAGGGTCCC
AAGCCCTGCAGTGCTACAGCTTTGAGCACACCTACTTTGGCCCCCTTTGACCTCAGGGCCATG
AAGCTGCCCAGCATCTCCTGTCCTCATGAGTGCTTTGAGGCTATCCTGTCTCTGGACACCGG
GTATCGCGCGCCGGTGACCCTGGTGCGGAAGGGCTGCTGGACCGGGCCTCCTGCGGGGCCAGA
CGCAATCGAACCCGGACGCGCTGCCGCCAGACTACTCGGTGGTGCGCGGCTGCACAACCTGAC
AAATGCAACGCCCCACCTCATGACTCATGACGCCCTCCCCAACCTGAGCCAAGCACCCGACCC
GCCGACGCTCAGCGGCGCCGAGTGCTACGCCTGTATCGGGGTCCACCAGGATGACTGCGCTA
TCGGCAGGTCCCGACGAGTCCAGTGTCACCAGGACCAGACCGCCTGCTTCCAGGGCAGTGGC
AGAATGACAGTTGGCAATTTCTCAGTCCCTGTGTACATCAGAACCTGCCACCGGCCCTCCTG
CACCACCGAGGGCACCACCAGCCCCCTGGACAGCCATCGACCTCCAGGGCTCCTGCTGTGAGG
GGTACCTCTGCAACAGGAAATCCATGACCCAGCCCTTCACCAGTGCTTCAGCCACCACCCCT
CCCCGAGCACTACAGGTCCTGGCCCTGCTCCTCCAGTCCTCCTGCTGGTGGGGCTCTCAGC
ATAGACCGCCCCCTCCAGGATGCTGGGGACAGGGCTCACACACCTCATTCTTGCTGCTTCAGC
CCCTATCACATAGCTCACTGGAAAATGATGTTAAAGTAAGAATTGCAAAA

56/75

FIGURE 56

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA86576
><subunit 1 of 1, 251 aa, 1 stop
><MW: 26935, pI: 7.42, NX(S/T): 2
MAMGVPRVILLCLFGAALCLTGSQALQCYSFEHTYFGPFDLRAMKLPSISCPHECFEAILSL
DTGYRAPVTLVRKGCWTGPPAGQTQSNPDALPPDYSVVRGCTTDKCNAHLMTHDALPNLSQA
PDPPTLSGAECYACIGVHQDDCAIGRSRRVQCHQDQTACFQSGRMTVGNFSVPVYIIRTCHR
PSCTTEGTTSPWTAIDLQGSCCEGYLCNRKSMTQPFTSASATTPPRALQVLALLLPVLLLVG
LSA

Important features of the protein:

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 233-251

N-glycosylation sites.

amino acids 120-124, 174-178

N-myristoylation sites.

amino acids 15-21, 84-90

57/75

FIGURE 57

GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCAGCCTCG
GCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCCCTGACTCCGTCCCGGCCAGGGAGGGC
CATGATTTCCCTCCCGGGGCCCCCTGGTGACCAACTTGCTGCGGTTTTTTGTTCTTGGGGCTGA
GTGCCCTCGCGCCCCCCTCGCGGGGCCAGCTGCAACTGCACTTGCCCCGCCAACCGGTTGCAG
GCGGTGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGCACGGGGAGGTGTCTTC
ATCCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAGAAAAGGAGGATC
AGGTGTTGTCCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTATCCTTGGTCTACTCC
ATGCCCTCCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGAAAGACTCTGGCCCCCTA
CAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGGCCACAGCATCAAAACCT
TAGAACTCAATGTACTGGTTCTTCCAGCTCCTCCATCCTGCCGTCTCCAGGGTGTGCCCCAT
GTGGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGGAGTAAGCCCGCTGTCCAATACCA
GTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTTGCACCAGCATTAGATGTCATCCGTG
GGTCTTTAAGCCTCACCAACCTTTCGTCTTCCATGGCTGGAGTCTATGTCTGCAAGGCCAC
AATGAGGTGGGCACTGCCCAATGTAATGTGACGCTGGAAGTGAGCACAGGGCCTGGAGCTGC
AGTGGTTGCTGGAGCTGTTGTGGGTACCCTGGTTGGACTGGGGTTGCTGGCTGGGCTGGTCC
TCTTGTACCACCGCCGGGGCAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCC
ATTGCTCCCCGGACCCTGCCCTGGCCCCAAGAGCTCAGACACAATCTCCAAGAATGGGACCCT
TTCCTCTGTCACCTCCGCACGAGCCCTCCGGCCACCCCATGGCCCTCCCAGGCCTGGTGCAT
TGACCCCCACGCCCAGTCTCTCCAGCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGAT
GGGGCCCACCCTCAACCAATATCCCCCATCCCTGGTGGGGTTTCTTCTCTGGCTTGAGCCG
CATGGGTGCTGTGCCTGTGATGGTGCCTGCCCAGAGTCAAGCTGGCTCTCTGGTAT**TGA**TGAC
CCCACCACTCATTGGCTAAAGGATTTGGGGTCTCTCCTTCTTATAAGGGTCACCTCTAGCAC
AGAGGCCTGAGTCATGGGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCCCACCTCTC
TTTACTGTGGGAAAACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGA
AGTGGATCTGGAATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTG
CTGAAATTAGCTACTACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCCAGGC
CCCCCTTGATCTGTACCCACCCCTATCTAACACCACCCCTTGGCTCCCACTCCAGCTCCCTGT
ATTGATATAACCTGTCAGGCTGGCTTGGTTAGGTTTTACTGGGGCAGAGGATAGGGAATCTC
TTATTAAACTAACATGAAATATGTGTTGTTTTTCATTTGCAAATTTAAATAAGATACATAA
TGTTTGTATGAAAAA

FIGURE 58

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGESS
 SQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKDSGPY
 SCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSQCSPRSKPAVQYQ
 WDRQLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLEVSTGPGAA
 VVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWKSSDTISKNGTL
 SSVTSARALRPPHGP RP GALTP T PSLSSQALPSPRLPTTDGAHPQPISPIPGGVSSSGLSR
 MGAVPVMVPAQSQAGSLV

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 245-267

N-glycosylation site.

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

N-myristoylation site.

amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,
 262-268, 308-314, 363-369, 364-370

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 164-175

FIGURE 59

ACTTGCCATCACCTGTTGCCAGTGTGGAAAAATTCTCCCTGTTGAATTTTTTGCACATGGAG
 GACAGCAGCAAAGAGGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGGAGATTATTTTAC
 CATACGCCCTCAGGACGTTCCCTCTAGCTGGAGTTCTGGACTTCAACAGAACCCCATCCAGT
 CATTTTGATTTTGCTGTTTATTTTTTTTTTCTTTTCTTTTCCCACCACATTGTATTTTAT
 TTCCGTACTTCAGAAATGGGCCTACAGACCACAAAGTGGCCCAGCCATGGGGCTTTTTTCCT
 GAAGTCTTGGCTTATCATTTCCTGGGGCTCTACTCACAGGTGTCCAACTCCTGGCCTGCC
 CTAGTGTGTGCCGCTGCGACAGGAACCTTGTCTACTGTAATGAGCGAAGCTTGACCTCAGTG
 CCTCTTGGGATCCCGGAGGGCGTAACCGTACTCTACCTCCACAACAACCAAATTAATAATGC
 TGGATTTCTGTCAGAACTGCACAATGTACAGTCGGTGCACACGGTCTACCTGTATGGCAACC
 AACTGGACGAATTCCCCATGAACCTTCCCAAGAATGTCAGAGTTCTCCATTTGCAGGAAAAC
 AATATTCAGACCATTTTACGGGCTGCTCTTGCCCAGCTCTTGAAGCTTGAAGAGCTGCACCT
 GGATGACAACTCCATATCCACAGTGGGGGTGGAAGACGGGGCCTTCCGGGAGGCTATTAGCC
 TCAAATTGTTGTTTTTGTCTAAGAATCACCTGAGCAGTGTGCCTGTTGGGCTTCCTGTGGAC
 TTGCAAGAGCTGAGAGTGGATGAAAATCGAATTGCTGTCATATCCGACATGGCCTTCCAGAA
 TCTCACGAGCTTGGAGCGTCTTATTGTGGACGGGAACCTCCTGACCAACAAGGGTATCGCCG
 AGGGCACCTTCAGCCATCTCACCAAGCTCAAGGAATTTTCAATTGTACGTAATTCGCTGTCC
 CACCCTCCTCCCGATCTCCCAGGTACGCATCTGATCAGGCTCTATTTGCAGGACAACCAGAT
 AAACCACATTCCTTTGACAGCCTTCTCAAATCTGCGTAAGCTGGAACGGCTGGATATATCCA
 ACAACCAACTGCGGATGCTGACTCAAGGGGTTTTTGATAATCTCTCCAACCTGAAGCAGCTC
 ACTGCTCGGAATAACCCTTGGTTTTGTGACTGCAGTATTAAATGGGTCACAGAATGGCTCAA
 ATATATCCCTTCATCTCTCAACGTGCGGGGTTTCATGTGCCAAGGTCCTGAACAAGTCCGGG
 GGATGGCCGTCAGGGAATTAAATATGAATCTTTTGTCTGTCCCACCACGACCCCCGGCCTG
 CCTCTCTTCACCCCAGCCCCAAGTACAGCTTCTCCGACCCTCAGCCTCCCACCCTCTCTAT
 TCCAAACCCTAGCAGAAGCTACACGCCTCCAACCTCCTACCACATCGAACTTCCCACGATTC
 CTGACTGGGATGGCAGAGAAAGAGTGACCCACCTATTTCTGAACGGATCCAGCTCTCTATC
 CATTTTGTGAATGATACTTCCATTCAAGTCAGCTGGCTCTCTCTCTTCCACCGTGATGGCATA
 CAACTCACATGGGTGAAAATGGGCCACAGTTTAGTAGGGGGGCATCGTTTCCAGGAGCGCATAG
 TCAGCGGTGAGAAGCAACACCTGAGCCTGGTTAACTTAGAGCCCCGATCCACCTATCGGATT
 TGTTTAGTGCCACTGGATGCTTTTAACTACCGCGCGGTAGAAGACACCATTTGTTTCCAGAGGC
 CACCACCCATGCCTCCTATCTGAACAACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGA
 CGTCCCACAGCATGGGCTCCCCCTTTCTGCTGGCGGGCTTGATCGGGGGCGCGGTGATATTT
 GTGCTGGTGGTCTTGCTCAGCGTCTTTTGTGCTGGCATATGCACAAAAAGGGGCGCTACACCTC
 CCAGAAGTGGAATACAACCGGGGCGGCGGAAAGATGATTATTGCGAGGCAGGCACCAAGA
 AGGACAACTCCATCCTGGAGATGACAGAAACCAGTTTTTCAGATCGTCTCCTTAAATAACGAT
 CAACTCCTTAAAGGAGATTTTCAAGTGCAGCCCATTTACACCCCAAATGGGGGCATTAATTA
 CACAGACTGCCATATCCCCAACAACATGCGATACTGCAACAGCAGCGTGCCAGACCTGGAGC
 ACTGCCATACGTGACAGCCAGAGGCCAGCGTTATCAAGGCGGACAATTAGACTCTTGAGAA
 CACACTCGTGTGTGCACATAAAGACACGCAGATTACATTTGATAAATGTTACACAGATGCAT
 TTGTGCATTTGAATACTCTGTAATTTATACGGTGTACTATATAATGGGATTTAAAAAAGTG
 CTATCTTTTCTATTTCAAGTTAATTACAAACAGTTTTTGTAACCTTTTGTCTTTTTTAAATCTT

FIGURE 60

MGLQTTKWPSHGAFFLKSWLIISLGLYSQVSKLLACPSVCRCDRNFVYCNERSLTSVPLGIP
 EGVTVLYLHNNQINNAGFPAELHNVQSVHTVYLYGNQLDEFPMNLPKNVRVLHLQENNIQTI
 SRAALAQLLKLEELHLDDNSISTVGVEDGAFREAIKLLFLSKNHLSSVPVGLPVDLQELR
 VDENRIAVISDMAFQNLTSLERLIVDGNLLTNKGIAEGTFSHLTKLKEFSIVRNSLSHPPPD
 LPGTHLIRLYLQDNQINHIPLTAFSNLRKLERLDISNNQLRMLTQGVFDNLSNLKQLTARNN
 PWFCDCSIKWVTEWLKYIPSSLNVRGFMCGPEQVRGMVRELMNLLSCPTTTPGLPLFTP
 APSTASPTTQPPTLSIPNPSRSYTPPTPTTSKLPPTIPDWDGRERVTPPISERIQLSIHFVND
 TSIQVSWLSLFTVMAYKLTWVKMGHSLVGGIVQERIVSGEKQHLSLVNLEPRSTYRICLVPL
 DAFNYRAVEDTICSEATTHASYLNNGSNTASSHEQTTSHSMGSPFLLAGLIGGAVIFVLVVL
 LSVFCWHMHKKGRYTSQKWKYNRGRRKDDYCEAGTKKDNSILEMTETSFQIVSLNNDQLLKG
 DFRLQPIYTPNGGINYTDCHIPNNMRYCNSSVPDLEHCHT

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 542-561

N-glycosylation site.

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

Casein kinase II phosphorylation site.

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

Tyrosine kinase phosphorylation site.

amino acids 319-328

N-myristoylation site.

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,
 522-528, 545-551, 633-639

Amidation site.

amino acids 581-585

Leucine zipper pattern.

amino acids 164-186

Phospholipase A2 aspartic acid active site.

amino acids 39-50

TGAGAGAGTAATAAGTTGGGAATCAAAAGAGTCAACGCAATGAACTGTTATTTACTGCTGCGTTT
TATGTTGGGAATTCCTCTCCTATGGCCTTGTCTTGGAGCAACAGAAAACCTCTCAAACAAAGA
AAGTCAAGCAGCCAGTGCGATCTCATTTGAGAGTGAAGCGTGGCTGGGTGTGGAACCAATTT
TTTGTACCAGAGGAAATGAATACGACTAGTCATCACATCGGCCAGCTAAGATCTGATTTAGA
CAATGGAAACAATTCTTTCCAGTACAAGCTTTTGGGAGCTGGAGCTGGAAGTACTTTTATCA
TTGATGAAAGAACAGGTGACATATATGCCATACAGAAGCTTGATAGAGAGGAGCGATCCCTC
TACATCTTAAGAGCCCAGGTAATAGACATCGCTACTGGAAGGGCTGTGGAACCTGAGTCTGA
GTTTGTTCATCAAAGTTTCGGATATCAATGACAATGAACCAAATTCCTAGATGAACCTTATG
AGGCCATTGTACCAGAGATGTCTCCAGAAGGAACATTAGTTATCCAGGTGACAGCAAGTGAT
GCTGACGATCCCTCAAGTGGTAATAATGCTCGTCTCCTCTACAGCTTACTTCAAGGCCAGCC
ATATTTTTCTGTTGAACCAACAACAGGAGTCATAAGAATATCTTCTAAAATGGATAGAGAAC
TGCAAGATGAGTATTGGGTAAATCATTCAAGCCAAGGACATGATTGGTCAGCCAGGAGCGTTG
TCTGGAACAACAAGTGTATTAATTAACTTTTCAGATGTTAATGACAATAAGCCTATATTTAA
AGAAAGTTTATACCGCTTGACTGTCTCTGAATCTGCACCCACTGGGACTTCTATAGGAACAA
TCATGGCATATGATAATGACATAGGAGAGAATGCAGAAATGGATTACAGCATTGAAGAGGAT
GATTCGCAAACATTTGACATTATTACTAATCATGAACTCAAGAAGGAATAGTTATATTAAA
AAAGAAAGTGGATTTTGTAGCACCAGAACCACTACGGTATTAGAGCAAAAGTTAAAAACCATC
ATGTTCCCTGAGCAGCTCATGAAGTACCACACTGAGGCTTCCACCCTTTCATTAAGATCCAG
GTGGAAGATGTTGATGAGCCTCCTCTTTTCCCTCCTTCCATATTATGTATTTGAAGTTTTTGA
AGAAACCCACAGGGATCATTTGTAGGCGTGGTGTCTGCCACAGACCCAGACAATAGGAAAT
CTCCTATCAGGTATTCTATTACTAGGAGCAAAGTGTTCAATATCAATGATAATGGTACAATC
ACTACAAGTAACTCACTGGATCGTGAAATCAGTGCTTGGTACAACCTAAGTATTACAGCCAC
AGAAAAATACAATATAGAACAGATCTCTTCGATCCCCTGTATGTGCAAGTTCTTAACATCA
ATGATCATGCTCCTGAGTTCTCTCAATACTATGAGACTTATGTTTGTGAAAATGCAGGCTCT
GGTCAGGTAATTCAGACTATCAGTGCGAGTGGATAGAGATGAATCCATAGAAGAGCACCATTT
TTACTTTAATCTATCTGTAGAAGACACTAACAATTCAAGTTTTTACAATCATAGATAATCAAG
ATAACACAGCTGTCAATTTTGACTAATAGAAGTGGTTTTAACCTTCAAGAAGAACCTGTCTTC
TACATCTCCATCTTAATTGCCGACAATGGAATCCCGTCACTTACAAGTACAAACACCCTTAC
CATCCATGTCTGTGACTGTGGTGACAGTGGGAGCACACAGACCTGCCAGTACCAGGAGCTTG
TGCTTTCCATGGGATTCAAGACAGAAGTTATCATTGCTATTCTCATTTGCATTATGATCATA
TTTGGGTTTTATTTTTTTGACTTTGGGTTTAAAACAACGGAGAAAACAGATTCTATTTCTGA
GAAAAGTGAAGATTTTCAGAGAGAATATATTTCCAATATGATGATGAAGGGGGTGGAGAAGAAG
ATACAGAGGGCCTTTGATATAGCAGAGCTGAGGAGTAGTACCATAATGCGGGAACGCAAGACT
CGGAAAACCAACAAGCGCTGAGATCAGGAGCCTATACAGGCAGTCTTTGCAAGTTGGCCCCGA
CAGTGCCATATTTCAGGAAATTCATTCTGGAAAAGCTCGAAGAAGCTAATACTGATCCGTGTG
CCCCTCCTTTTGATTCCCTCCAGACCTACGCTTTTGTAGGGAACAGGGTCATTAGCTGGATCC
CTGAGCTCCTTAGAATCAGCAGTCTCTGATCAGGATGAAAGCTATGATTACCTTAATGAGTT
GGGACCTCGCTTTAAAAGATTAGCATGCATGTTTGCTTCTGCAGTGCAGTCAAATAATTAGG
GCTTTTTTACCATCAAATTTTTTAAAAGTGCTAATGTGTATTTCGAACCCAATGGTAGTCTTAA
AGAGTTTTGTGCCCTGGCTCTATGGCGGGGAAAGCCCTAGTCTATGGAGTTTTCTGATTTCC
CTGGAGTAAATACTCCATGGTTATTTTAAAGCTACCTACATGCTGTCAATTGAACAGAGATGTG
GGGAGAAATGTAAACAATCAGCTCACAGGCATCAATACAACCAGATTTGAAGTAAATAATG
TAGGAAGATATTTAAAAGTAGATGAGAGGACACAAGATGTAGTCGATCCTTATGCGATTATAT
CATTATTTACTTAGGAAAGAGTAAAAATACCAAACGAGAAAATTTAAAGGAGCAAAAATTTG
CAAGTCAAATAGAAATGTACAAATCGAGATAACATTTACATTTCTATCATATTGACATGAAA
ATTGAAAATGTATAGTCAGAGAAATTTTCATGAATTATTCATGAAGTATTGTTTCCTTTAT
TTAAA

FIGURE 62

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53906

><subunit 1 of 1, 772 aa, 1 stop

><MW: 87002, pI: 4.64, NX(S/T): 8

MNCYLLLRFMLGIPLLPCLGATENSQTKKVKQPVRSHLRVKRGWVWNQFFVPEEMNTTSHH
 IGQLRSDLDNGNNSFQYKLLGAGAGSTFIIDERTGDIYAIQKLDREERSLYILRAQVIDIAT
 GRAVEPESEFVIKVSNDINDNEPKFLDEPYEAIVPMSPEGTLVIQVTASDADDPSSGNNARL
 LYSLLQGQPYFSVEPTTGVIRISSKMDRELQDEYWVIIQAKDMIGQPGALSGTTSVLIKLS
 VNDNKPIFKESLYRLTVSESAPTGTSGTIMAYDNDIGENAEMDYSIEEDDSQTFDIITNHE
 TQEGIVILKKKVDFEHQNHYGIRAKVKNHHVPEQLMKYHTEASTTFIKIQVEDVDEPPLFL
 PYYVFEVFEETPQGSFVGVSATDPDNRKSPIRYSITRSKVFNINDNGTITTSNSLDREISA
 WYNLSITATEKYNIEQISSIPLYVQVLNINDHAPEFSQYYETYVCENAGSGQVIQTI
 SAVDR
 DESIEEHFHYFNLSVEDTNSSFTIIDNQDNTAVILTNRTGFNLQEEPVFYISILIADNGIP
 SLTSTNTLTIHVCDGDSGSTQTCQYQELVLSMGFKTEVIIAILICIMIIFGFIFLTLGLKQ
 RRKQILFPEKSEDFRENI
 FQYDDEGGGEEDTEAFDIAELRSSTIMRERKTRKTTSAEIRSLY
 RQSLQVGPDSAIFRKFILEKLEEANTDPCAPPFDSLQTYAFEGTGSLAGSLSSLES
 SAVSDQD
 ESYDYLNELGPRFKRLACMFGSAVQSNN

Important features:**Signal peptide:**

amino acids 1-21

Transmembrane domain:

amino acids 597-617

N-glycosylation sites.

amino acids 57-60, 74-77, 419-423, 437-440, 508-511, 515-518,
 516-519 and 534-537

Cadherins extracellular repeated domain signature.

amino acids 136-146 and 244-254

FIGURE 63

CTTCAGAACAGGTTCTCCTTCCCCAGTCACCAGTTGCTCGAGTTAGAATTGTCTGCAATGGC
CGCCCTGCAGAAATCTGTGAGCTCTTTCCTTATGGGGACCCTGGCCACCAGCTGCCTCCTTC
TCTTGGCCCTCTTGGTACAGGGAGGAGCAGCTGCGCCCATCAGCTCCCAGTGCAGGCTTGAC
AAGTCCAACCTCCAGCAGCCCTATATCACCAACCGCACCTTCATGCTGGCTAAGGAGGCTAG
CTTGGCTGATAACAACACAGACGTTTCGTCTCATTGGGGAGAACTGTTCCACGGAGTCAGTA
TGAGTGAGCGCTGCTATCTGATGAAGCAGGTGCTGAACTTCACCCTTGAAGAAGTGCTGTTC
CCTCAATCTGATAGGTTCCAGCCTTATATGCAGGAGGTGGTGCCCTTCCTGGCCAGGCTCAG
CAACAGGCTAAGCACATGTCATATTGAAGGTGATGACCTGCATATCCAGAGGAATGTGCAA
AGCTGAAGGACACAGTGAAAAAGCTTGGAGAGAGTGGAGAGATCAAAGCAATTGGAGAACTG
GATTTGCTGTTTATGTCTCTTGAGAAATGCCTGCATTTGACCAGAGCAAAGCTGAAAAATGAA
TAACTAACCCCTTTCCCTGCTAGAAATAACAATTAGATGCCCCAAAGCGATTTTTTTTAAAC
CAAAAGGAAGATGGGAAGCCAACTCCATCATGATGGGTGGATTCCAAATGAACCCCTGCGT
TAGTTACAAAGGAAACCAATGCCACTTTTGTTTATAAGACCAGAAGGTAGACTTTCTAAGCA
TAGATATTTATTGATAACATTTTCATTGTAAGTGGTGTCTATACACAGAAAACAATTTATTT
TTTAAATAATTGTCTTTTTTCCATAAAAAAGATTACTTTCCATTCCTTTAGGGGAAAAAACCC
CTAAATAGCTTCATGTTTCCATAATCAGTACTTTATATTTATAAATGTATTTATTATTATTA
TAAGACTGCATTTTATTTATATCATTTTATTAATATGGATTTATTTATAGAAACATCATTCG
ATATTGCTACTTGAGTGTAAGGCTAATATTGATATTTATGACAATAATTATAGAGCTATAAC
ATGTTTATTTGACCTCAATAAACACTTGGATATCCC

FIGURE 64

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA125185

><subunit 1 of 1, 179 aa, 1 stop

><MW: 20011, pI: 8.10, NX(S/T): 3

MAALQKSVSSFLMGTLATSCLLLLALLVQGGAAAPISSHCRLDKSNFQQPYITNRTFMLAKE
ASLADNNTDVRLIGEKLFGVSMSERCYLMKQVLNFTLEEVLPQSDRFQPYMQEVVPFLAR
LSNRLSTCHIEGDDLHIQRNVQKLKDTVKKLGESGEIKAIGELDLLFMSLRNACI

Important features of the protein:**Signal peptide:**

amino acids 1-33

N-glycosylation sites.

amino acids 54-58, 68-72, 97-101

N-myristoylation sites.

amino acids 14-20, 82-88

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 10-21

FIGURE 65

GCCCTAACCTTCCCAGGGCTCAGCTCTTTGGAGCTGCCCATTCCTCCGGCTGCGAGAAAGGA
CGCGCGCCCTGCGTCGGGCGAAGAAAAGAAGCAAACTTGTCGGGAGGGTTTCGTCAACAAC
CTCCTTCCCGCAAACCTAAACCTCCTGCCGGGGCCATCCCTAGACAGAGGAAAGTTCCTGCA
GAGCCGACCAGCCCTAGTGGATCTGGGGCAGGCAGCGGCGCTGGCTGTGGAATTAGATCTGT
TTTGAACCCAGTGGAGCGCATCGCTGGGGCTCGGAAGTCACCGTCCGCGGGCACCGGGTTGG
CGCTGCCCCGAGTGGAACCGACAGTTTGCGAGCCTCGGCTGCAAGTGGCCTCTCCTCCCCGCG
GTTGTTGTTCAGTGTGCGGGTGAGGGCTGCGAGTGTGGCAAGTTGCAAAGAGAGCCTCAGAGG
TCCGAAGAGCGCTGCGCTCCTACTCGCGTTTCGCTTCTTCTCCTCCTCCTCGGTTCCCTACTGTGA
AATCGCAGCGACATTTACAAAGGCCTCCGGGTCTACCGAGACCGATCCGCAGCGTTTGGCC
CGGTTCGTGCCTATTGCATCGGGAGCCCCGAGCACCGGCGAAATGCGGAGGTTCCCGAAGGC
CGACCTGGCCGCTGCAGGAGTTATGTTACTTTGCCACTTCTTCACGGACCAGTTTCAGTTCG
CCGATGGGAAACCCGGAGACCAAATCCTTGATTGGCAGTATGGAGTTACTCAGGCCTTCCCT
CACACAGAGGAGGAGGTGGAAGTTGATTCACACGCGTACAGCCACAGGTGGAAAAGAACTT
GGACTTTCTCAAGGCGGTAGACACGAACCGAGCAAGCGTCGGCCAAGACTCTCCTGAGCCCA
GAAGCTTCACAGACCTGCTGCTGGATGATGGGCAGGACAATAACACTCAGATCGAGGAGGAT
ACAGACCACAATTACTATATATCTCGAATATATGGTCCATCTGATTCTGCCAGCCGGGATT
ATGGGTGAACATAGACCAAATGGAAAAAGATAAAGTGAAGATTCATGGAATATTGTCCAATA
CTCATCGGCAAGCTGCAAGAGTGAATCTGTCTTCGATTTTCCATTTTATGGCCACTTCCTA
CGTGAAATCACTGTGGCAACCGGGGGTTTCATATACACTGGAGAAGTCGTACATCGAATGCT
AACAGCCACACAGTACATAGCACCTTTAATGGCAAATTTTCGATCCCAGTGTATCCAGAAATT
CAACTGTCAGATATTTTGATAATGGCACAGCACTTGTGGTCCAGTGGGACCATGTACATCTC
CAGGATAATTATAACCTGGGAAGCTTCACATTCCAGGCAACCCTGCTCATGGATGGACGAAT
CATCTTTGGATACAAAGAAATTCCTGTCTTGGTCCACACAGATAAGTTCAACCAATCATCCAG
TGAAAGTCGGACTGTCCGATGCATTTGTCTGTCCACAGGATCCAACAAATTCCTCAATGTT
CGAAGAAGAACAATTTATGAATACCACCGAGTAGAGCTACAAATGTCAAAAATTACCAACAT
TTCGGCTGTGGAGATGACCCCATTAACCCACATGCCTCCAGTTTAACAGATGTGGCCCCCTGTG
TATCTTCTCAGATTGGCTTCAACTGCAGTTGGTGTAGTAAACTTCAAAGATGTTCCAGTGGA
TTTGATCGTCATCGGCAGGACTGGGTGGACAGTGGATGCCCTGAAGAGTCAAAGAGAGAAGAT
GTGTGAGAATACAGAACCAGTGGAACTTCTTCTCGAACCACCACAACCGTAGGAGCGACAA
CCACCCAGTTCAGGGTCTTAACCTACCACCAGAAGAGCAGTGACTTCTCAGTTTCCCACCAGC
CTCCCTACAGAAGATGATACCAAGATAGCACTACATCTAAAAGATAATGGAGCTTCTACAGA
TGACAGTGCAGCTGAGAAGAAAGGGGGAACCCTCCACGCTGGCCTCATCATTGGAATCCTCA
TCCTGGTCTCTATTGTAGCCACAGCCATTCTTGTGACAGTCTATATGTATCACCACCCAACA
TCAGCAGCCAGCATCTTCTTTATTGAGAGACGCCCAAGCAGATGGCCTGCGATGAAGTTTAG
AAGAGGCTCTGGACATCCTGCCTATGCTGAAGTTGAACCAGTTGGAGAGAAAGAAGGCTTTA
TTGTATCAGAGCAGTGCATAAATTTCTAGGACAGAACACACCAGTACTGGTTTACAGGTGT
TAAGACTAAAATTTTGCCTATACCTTTAAGACAAACAAACAAACACACACAAACAAAGCTC
TAAGCTGCTGTAGCCTGAAGAAGACAAGATTTCTGGACAAGCTCAGCCCAGGAAACAAAGGG
TAAACAAAAAACTAAAATTTATACAAGATAACATTTTACACTGAACATAGAATTCCCTAGTGG
AATGTCATCTATAGTTCACCTCGGAACATCTCCCGTGGACTTATCTGAAGTATGACAAGATTA
TAATGCTTTTGGCTTAGGTGCAGGGTTGCAAAGGGATCAGAAAAAAAATCATAATAAAGC
TTTAGTTCATGAGGG

FIGURE 66

MARFPKADLAAAGVMLLCHFFTDQFQFADGKPGDQILDWQYGVQTQAFPHTEEEVEVDSHAYS
HRWKRNLDFLKAVDTNRASVGQDSPEPRSFTDLLLDDGQDNNTQIEEDTDHNYYISRIYGPS
DSASRDLWVNIDQMEKDKVKIHGILSNTHRQAARVNLSFDFPFYGHFLREITVATGGFIYTG
EVVHRMLTATQYIAPLMANFDPSVSRNSTVRYFDNGTALVVQWDHVHLQDNYNLGSFTFQAT
LLMDGRIIFGYKEIPVLVTQISSTNHPVKVGLSDAFVVVHRIQQIPNVRRRTIYEHVRELQ
MSKITNISAVEMTLPPTCLQFNRCGPCVSSQIGFNCSCWCSKLQRCSSGFDRHRQDWVDSGCP
EESKEKMCENTEPVETSSRTTTTVGATTTQFRVLTTRRAVTSQFPTSLPTEDDTKIALHLK
DNGASTDDSAAEKKGGTLHAGLIIGILILVLIVATAILVTVMYHHPTSAAASIFFIERRPSR
WPAMKFRRGSGHPAYAEVEPVGEKEGFIVSEQC

Important features of the protein:**Transmembrane domain:**

amino acids 454-478

N-glycosylation sites.

amino acids 103-107, 160-164, 213-217, 221-225, 316-320, 345-349

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 297-301, 492-496, 503-507

N-myristoylation sites.

amino acids 42-48, 100-106, 147-153, 279-285, 397-403, 450-456,
455-461

67/75

68/75

FIGURE 67B

AGTGGTGCTACCACAAAAAATGTTAACCATCAGTACCATTGTTTGGGAGAAAGAAACAGATC
AAGAATGCATATTATTTCAGTGACCGCTTTCCTAGAGTTAAAATACCTCCTCTTTGTAAGGTT
TGTAGGTAAATTGAGGTATAAACTATGGATGAACCAAATAATTAGTTCAAAGTGTTGTCATG
ATTCCAAATTTGTGGAGTCTGGTGTTTTTACCATAGAATGTGACAGAAGTACAGTCATAGCT
CAGTAGCTATATGTATTTGCCTTTATGTTAGAAGAGACTTTCTTGAGTGACATTTTTTAAATA
GAGGAGGTATTCACATATGTTTTTCTGTATCACAGCAGCATTCCTAGTCCTTAGGCCCTCGGA
CAGAGTGAAATCATGAGTATTTATGAGTTCAATATTGTCAAATAAGGCTACAGTATTTGCTT
TTTTGTGTGAATGTATTGCATATAATGTTCAAGTAGATGATTTTACATTTTATGGACATATAA
AATGTCTGATTACCCCATTTTATCAGTCCTGACTGTACAAGATTGTTGCAATTTTCAGAATAG
CAGTTTTTATAAATTGATTTATCTTTTAATCTATAACAATTTGTGTTAGCTGTTTCAATTTTCAGG
ANTATATTTTCTACAAGTTCCACTTGTGGGACTCCTTTTGTGCCCCCTATTTTTTTTTTAAAG
AAGGAAGAAAGAAAAATAAGTAGCAGTTTAAAAATGAGAATGGAGAGAAAAGAAAAAGAATG
AAAAGGAAAGGCAGTAAAGAGGGAAAAAAAAGGAAGGATGGAAGGAATGAAGGAAGGAAGGG
AGGAAGGGGAGAAGGTAGGAAGAAAGAAAGGATGAGAGGGGAAGGAAGAATCAGAGTATTAGG
GTAGTTAACTTACACATTTGCATTCTTAGTTTAACTGCAAGTGGTGTAAGTATGTTTTTCAA
TGATCGCATTTGAAACATAAGTCCTATTATACCATTAAAGTTCCTATTATGCAGCAATTATAT
AATAAAAAGTACTGCCCAAGTTATAGTAATGTGGGTGTTTTTGGAGACACTAAAAGATTTGAG
AGGGAGAATTTCAAACCTTAAAGCCACTTTTGGGGGGTTTATAACTTAACTGAAAAATTAATG
CTTCATCATAACATTTAAGCTATATCTAGAAAGTAGACTGGAGAACTGAGAAAATTACCCAG
GTAATTCAGGGGAAAAAAAAAATATATATATATATAAATACCCCTACATTTGAAGTCAGAAA
ACTCTGAAAACTGAATTATCAAAGTCAATCATCTATAATGATCAAATTTACTGAACAATTG
TTAATTTATCCATTGTGCTTAGCTTTGTGACACAGCCAAAAGTTACCTATTTAATCTTTTCA
ATAAAAATTGTTTTTTGAAATCCAGAAATGATTTAAAAAGAGGTCAGGTTTTTAACTATTTA
TTGAAGTATGTGGATGTACAGTATTTCAATAGATATGAATATGAATAAATGGTATGCCTTAA
GATTCTTTGAATATGTATTTACTTTAAAGACTGGAAAAAGCTCTTCCTGTCTTTTAGTAAAA
CATCCATATTTTCATAACCTGATGTAAAATATGTTGTACTGTTTCCAATAGGTGAATATAAAC
TCAGTTTATCAATTAAAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA

70/75

FIGURE 69

ATAGTAGAAGAATGTCTCTGAAATTACTGGATGAGTTTCAGTCATACTTTCACATGGGCACA
 ATTCACATTCAAGCTCCTTATCCTAGGCTAATTTTATATTATGTTAAATCACTTGTTTTG
 TTCTCACGGCTTCCTGCCTGCTATAGGCATAATTACGAGGAAGCAGAACTTCTCCAGAAGCA
 AGCGCACATGCGTTCCAAAATAAGAGCAAATTCGCTCTAAACACAGGAAAAGACCTGAAGCT
 TTAATTAAGGGGTACATCCAACCCAGAGCGCTTTTGTGGGCACTGATTGCTCCAGCTTCT
 GCGTCACTGCGCGAGGGAAGAGGGAAGAGGATCCAGGCGTTAGACATGTATAGACACAAAAA
 CAGCTGGAGATTGGGCTTAAAATACCCACCAAGCTCCAAAGAAGAGACCCAAGTCCCCAAAA
 CATTGATTTTCAGGGCTGCCAGGAAGGAAGAGCAGCAGCAGGGTGGGAGAGAAGCTCCAGTCA
 GCCACAAGATGCCATTGTCCCCGGCCTCCTGCTGCTGCTGCTCTCCGGGGCCACGGCCAC
 CGCTGCCCTGCCCTGGAGGGTGGCCCCACCGGCCGAGACAGCGAGCATATGCAGGAAGCGG
 CAGGAATAAGGAAAAGCAGCCTCCTGACTTTCCTCGCTTGGTGGTTTGAGTGGACCTCCCAG
 GCCAGTGCCGGGGCCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAGGCGC
 ACCCCCCCAGCAATCCGCGCGCCGGGACAGAATGCCCTGCAGGAACTTCTTCTGGAAGACCT
 TCTCCTCCTGCAAATAG

71/75

FIGURE 70

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA44175

><subunit 1 of 1, 155 aa, 1 stop

><MW: 17194, pI: 10.44, NX(S/T): 0

MYRHKNSWRLGLKYPPSSKEETQVPKTLISGLPGRKSSSRVGEKLQSAHKMPLSPGLLLLLLL
SGATATAALPLEGGPTGRDSEHMQEAAGIRKSSLLTFLAWWFEWTSQASAGPLIGEEAREVA
RRQEGAPPQQSARRDRMPCRNFFWKTFSSCK

Important features of the protein:

Transmembrane domain:

amino acids 51-69

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 35-39, 92-96

N-myristoylation sites.

amino acids 64-70, 75-81, 90-96

Amidation site.

amino acids 33-37

FIGURE 71

GTCGTGTGCTTGGAGGAAGCCGCGGAACCCCCAGCGTCCGTCC**ATG**GCGTGGAGCCTTGGGA
GCTGGCTGGGTGGCTGCCTGCTGGTGTGAGCATTGGGAATGGTACCACCTCCCGAAAATGTC
AGAATGAATTCTGTTAATTTCAAGAACATTCTACAGTGGGAGTCACCTGCTTTTGCCAAAGG
GAACCTGACTTTCACAGCTCAGTACCTAAGTTATAGGATATTCCAAGATAAATGCATGAATA
CTACCTTGACGGAATGTGATTTCTCAAGTCTTTCCAAGTATGGTGACCACACCTTGAGAGTC
AGGGCTGAATTTGCAGATGAGCATTGAGACTGGGTAAACATCACCTTCTGTCCTGTGGATGA
CACCATTATTGGACCCCCCTGGAATGCAAGTAGAAGTACTTGCTGATTCTTTACATATGCGTT
TCTTAGCCCCCTAAAATTGAGAATGAATACGAACTTGGACTATGAAGAATGTGTATAACTCA
TGGACTTATAATGTGCAATACTGGAAAAACGGTACTGATGAAAAGTTTCAAATTACTCCCCA
GTATGACTTTGAGGTCCTCAGAAACCTGGAGCCATGGACAACCTTATTGTGTTCAAGTTCGAG
GGTTTCTTCCTGATCGGAACAAAGCTGGGGAATGGAGTGAGCCTGTCTGTGAGCAAACAACC
CATGACGAAACGGTCCCCCTCCTGGATGGTGGCCGTCATCCTCATGGCCTCGGTCTTCATGGT
CTGCCTGGCACTCCTCGGCTGCTTCTCCTTGCTGTGGTGCCTTTACAAGAAGACAAAGTACG
CCTTCTCCCCTAGGAATTCTCTTCCACAGCACCTGAAAGAGTTTTTGGGCCATCCTCATCAT
AACACACTTCTGTTTTTCTCCTTTCCATTGTCGGATGAGAATGATGTTTTTGGACAAGCTAAG
TGTCATTGCAGAAGACTCTGAGAGCGGCAAGCAGAATCCTGGTGACAGCTGCAGCCTCGGGA
CCCCGCCTGGGCAGGGGCCCCAAAGC**TAG**GCTCTGAGAAGGAAACACACTCGGCTGGGCACA
GTGACGTAATCCATCTCACATCTGCCTCAGTGAGGGATCAGGGCAGCAAACAAGGGCCAAGA
CCATCTGAGCCAGCCCCACATCTAGAACTCCAGACCTGGACTTAGCCACCAGAGAGCTACAT
TTTAAAGGCTGTCTTGGCAAAAATACTCCATTTGGGAACTCACTGCCTTATAAAGGCTTTCA
TGATGTTTTTCAGAAGTTGGCCACTGAGAGTGTAATTTTCAGCCTTTTATATCACTAAAATAA
GATCATGTTTTAATTGTGAGAAACAGGGCCGAGCACAGTGGCTCACGCCTGTAATACCAGCA
CCTTAGAGGTCGAGGCAGGCGGATCACTTGAGGTCAGGAGTTCAAGACCAGCCTGGCCAATA
TGGTGAAACCCAGTCTCTACTAAAAATACAAAAATTAGCTAGGCATGATGGCGCATGCCTAT
AATCCCAGCTACTCGAGTGCCTGAGGCAGGAGAATTGCATGAACCCGGGAGGAGGAGGAGGA
GGTTGCAGTGAGCCGAGATAGCGGCACTGCACTCCAGCCTGGGTGACAAAGTGAGACTCCAT
CTCAAAAAAAAAAAAAAAAAAATTGTGAGAAACAGAAATACTTAAAATGAGGAATAAGAATGG
AGATGTTACATCTGGTAGATGTAAACATTCTACCAGATTATGGATGGACTGATCTGAAAATCG
ACCTCAACTCAAGGGTGGTCAGCTCAATGCTACACAGAGCACGGACTTTTGGAATCTTTGCA
GTACTTTGAATTTATTTTTCTACCTATATATGTTTTATATGCTGCTGGTGCTCCATTAAAGT
TTTACTCTGTGTTGC

73/75

FIGURE 72

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83551
><subunit 1 of 1, 325 aa, 1 stop
><MW: 37011, pI: 5.09, NX(S/T): 4
MAWSLGSWLGGCLLVSALGMVPPPENVRMNSVNFKNILQWESPAFAKGNLTFTAQYLSYRIF
QDKCMNTTLTECDFSSLSKYGDHTLRVRAEFADEHSDWVNITFCPVDDTIIGPPGMQVEVLA
DSLHMRFLAPKIENEYETWTMKNVYNSWTYNVQYWKNGTDEKFQITPQYDFEVLRLNLEPWTT
YCVQVRGFLPDRNKAGEWSEPVCEQTTHDETVPSPWMVAVILMASVFMVCLALLGCFSLLWCV
YKKT KYAFSPRNSLPQHLKEFLGHPHNTLLFFSFPLSDENDVFDKLSVIAEDSESGKQNPG
DSCSLGTTPPGQGPQS
```

Important features of the protein:

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 222-245

N-glycosylation sites.

amino acids 49-53, 68-72, 102-106, 161-165

N-myristoylation sites.

amino acids 6-12, 316-322

FIGURE 73

CGAGCGCCAACCCGCTAGCGCCTGAATCCGGCGTGCTGCCCGCTCGCCGCCCGCC**ATGGCCC**
GCGCAGCCCCGCTGCTCGCCGCGTTGACCGCGCTCCTCGCCGCCCGCGCTGCTGGCGGAGAT
GCCCCGCCGGGCAAAATCGCGGTGGTTGGGGCTGGGATTGGGGGCTCTGCTGTGGCCCATTT
TCTCCAGCAGCACTTTGGACCTCGGGTGCAGATCGACGTGTACGAGAAGGGAACCGTGGGTG
GCCGCTTGGCCACCATCTCAGTCAACAAGCAGCACTATGAGAGCGGGGCTGCCTCCTTCCAC
TCCCTGAGCCTGCACATGCAGGACTTCGTCAAGCTGCTGGGGCTGAGGCACCGGCGCGAGGT
GGTGGGCAGGAGCGCCATCTTCGGCGGGGAGCACTTCATGCTGGAGGAGACTGACTGGTACC
TGCTGAACCTCTTCCGCCTCTGGTGGCACTATGGCATCAGCTTCCTGAGGCTGCAGATGTGG
GTGGAGGAGGTGATGGAGAAGTTCATGAGGATCTATAAGTACCAGGCCACGGCTATGCCTT
CTCGGGTGTGGAGGAGCTGCTCTACTCACTGGGGGAGTCCACCTTTGTAAACATGACCCAGC
ACTCTGTGGCTGAGTCCCTGCTGCAGGTGGGCGTCACGCAGCGCTTTATTGATGATGTCGTT
TCTGCTGTCCTGCGGGCCAGCTATGGCCAGTCAGCAGCGATGCCCGCCTTTGCAGGAGCCAT
GTCACTAGCCGGGGGCCCAAGGCAGCCTGTGGTCTGTGGAAGGAGGCAATAAGCTGGTTTGT
CCGTTTGTGCTGAAGCTCACCAAGGCCAATGTGATCCATGCCACAGTGACCTCTGTGACCCTG
CACAGCACAGAGGGGAAAGCCCTGTACCAGGTGGCGTATGAGAATGAGGTAGGCAACAGCTC
TGACTTCTATGACATCGTGGTCATCGCCACCCCCCTGCACCTGGACAACAGCAGCAGCAACT
TAACCTTTGCAGGCTTCCACCCGCCCAATTGATGACGTGCAGGGCTCTTTCCAGCCCACCGTC
GTCTCCTTGGTCCACGGCTACCTCAACTCGTCTTACTTCGGTTTCCCAGACCCTAAGCTTTT
CCCCTTTGCCAACATCCTTACCACAGATTTCCCCAGCTTCTTCTGCACTCTGGACAACATCT
GCCCTGTCAACATCTCTGCCAGCTTCCGGCGAAAGCAGCCCCAGGAGGCAGCTGTTTGGCGA
GTCCAGTCCCCCAAGCCCTCTTTTCGGACCCAGCTAAAGACCCTGTTCCGTTCTTACTC
AGTGCAGACAGCTGAGTGGCAGGCCCATCCCCTCTATGGCTCCCGCCCCACGCTCCCGAGGT
TTGCACTCCATGACCAGCTCTTCTACCTCAATGCCCTGGAGTGGGCGGCCAGCTCCGTGGAG
GTGATGGCCGTGGCTGCCAAGAATGTGGCCTTGCTGGCTTACAACCGCTGGTACCAGGACCT
AGACAAGATTGATCAAAAAGATTTGATGCACAAGGTCAAGACTGAACTGTGAGGGCTCTAGG
GAGAGCCTGGGAACTTTCATCCCCACTGAAGATGGATCATCCACAGCAGCCCAGGACTGA
ATAAGCCATGCTCGCCCACCAGGCTTCTTTCTGACCCCTCATGTATCAAGCATCTCCAGGTG
ACCTACTGTCTGCCTATATTAAGGGTCCACACGGCGGCTGCTGCTTTTTTTTTTAAGGGGAAA
GTAAGAAAAGAGAAGGAAATCCAAGCCAGTATATTTGTTTTATTTATTTTTTTTAAGAAGAA
AAAAGTTCATCTTCACAAGGTGCTTCAGACTTGGTTTCTTAGCTAGAAACCAGAAGACTACG
GGAGGGAATATAAGGCAGAGAACTATGAGTCTTATTTTATTACTGTTTTTCACTACCTACTC
CCACAATGGACAATCAATTGAGGCAACCTACAAGAAAACATTTACAACCAGATGGTTACAAA
TAAAGTAGAAGGGAAGATCAGAAAACCTAAGAAATGATCATAGCTCCTGGTTACTGTGGACT
TGATGGATTTGAAGTACCTAGTTCAGAACTCCCTAGTCACCATCTCCAAGCCTGTCAACATC
ACTGCATATTGGAGGAGATGACTGTGGTAGGACCCAAGGAAGAGATGTGTGCCTGAATAGTC
GTCACCATATCTCCAAGCTTCCTGGCAACCAGTGGGAAAAGAAACATGCGAGGCTGTAGGAA
GAGGGAAGCTCTTCCTTGGCACCTAGAGGAATTAGCCATTCTCTTCCTTATGCAAAGATTGA
GGAATGCAACAATATAAAGAAGAGAAGTCCCCAGATGGTAGAGAGCAGTCATATCTTACCCC
TAGATGTTTCATCCCAGCAGAAGAAAGAAGAGGTGTTGGGGTAGGATTCTTCAGAGGTAGC
CTGGTACTTTCTCATCAGACACTAGCTTGAAGTAAGAGGAGAATTATGCTTTTCTTTGCTTT
TTCTACAAACCCTTAAAAATCACTTGTTTTAAAAAGAAAGTAAAGCCCTTTTCATTCAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 74

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA116510
><subunit 1 of 1, 494 aa, 1 stop
><MW: 54646, pI: 7.27, NX(S/T): 6
MARAAPLLAALTALLAAAAAGGDAPPGKIAVVGAGIGGSAVAHFLQQHFGPRVQIDVYEKGT
VGGRLATISVNBKQHYESGAASFHSLSLHMQDFVKLLGLRHRREVVGRSAIFGGEHFMLEETD
WYLLNLFRLWWHYGISFLRLQMWVEEVMEKFMRIYKYQAHGYAFSGVEELLYSLGESTFVNM
TQHSVAESLLQVGVTQRFIDDVSAVLRASYGQSAAMPAFAGAMSLAGAQQGSLWSVEGGNKL
VCSGLLKLTKANVIHATVTSVTLHSTEGKALYQVAYENEVGNSSDFYDIVVIATPLHLDNSS
SNLTFAGFHPPIDDVQGSFQPTVVSLVHGYLNSSYFGFPDPKLFPPFANILTTDFPSFFCTLD
NICPVNISASFRRKQPQEAADVWRVQSPKPLFRTQLKTLFRSYYSVQTAEWQAHPYGSRPTL
PRFALHDQLFYLNLEWAASSVEVMAVAANKVALLAYNRWYQDLDKIDQKDLMHKVKTEL

Important features of the protein:**Signal peptide:**

amino acids 1-19

N-glycosylation sites.

amino acids 185-189, 290-294, 308-312, 312-316, 342-346, 378-382

N-myristoylation sites.

amino acids 33-39, 35-41, 38-44, 61-67, 64-70, 218-224, 234-240,
237-243, 429-435